

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2005, 10:37:22 ; Search time 405 Seconds  
(without alignments)  
13023.431 Million cell updates/sec

Title: US-09-786-867C-1

Perfect score: 891

Sequence: 1 ttgacaccagacactggt.....acgacacacataaaaaaa 891

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0\$  
Maximum Match 100\$  
Listing first 45 summaries

Database : N Geneseq 16Dec04:\*  
1: Geneseqn1980a:\*  
2: Geneseqn1990a:\*  
3: Geneseqn2000a:\*  
4: Geneseqn2001a:\*  
5: Geneseqn2001b:\*  
6: Geneseqn2002a:\*  
7: Geneseqn2002b:\*  
8: Geneseqn2003a:\*  
9: Geneseqn2003b:\*  
10: Geneseqn2003c:\*  
11: Geneseqn2003d:\*  
12: Geneseqn2004a:\*  
13: Geneseqn2004b:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	891	100.0	891	3	AAAI3648 Human onc
2	864.8	97.1	891	3	AAAI3614 Human onc
3	861.6	96.7	891	3	AAAI3615 Human onc
4	852	95.6	868	3	AAAI3647 Human onc
5	373.8	42.0	567	6	Abk55135 Human col
6	373.8	42.0	583	9	Ach40379 Human foe
7	373.8	42.0	630	12	Adq84434 Human tum
8	373.8	42.0	630	12	Adq83261 Human tum
9	373.8	42.0	630	13	Adq85218 Human tum
10	373.8	42.0	630	13	Acn39230 Tumour-as
11	373.8	42.0	790	4	Aah02927 Human she
12	373.8	42.0	801	12	Adq29634 Human col
13	373.8	42.0	801	13	Adp24690 PRO polyp
14	373.8	42.0	830	11	Acn88431 Breast ca
15	373.8	42.0	920	4	Aah23073 Osteoarth
16	373.8	42.0	998	8	Acn03888 cDNA upre
17	373.8	42.0	1078	6	Abn59686 Novel hum
18	373.8	42.0	1326	8	ACA03889 cDNA upre
19	373.8	42.0	2311	8	Acc46705 Human dit
20	373.4	41.9	791	6	Abk55442 Human col

21	373	41.9	1119	8	Abz71972	Human fer
22	373	41.9	1198	6	Abk83853	Human CDN
23	373	41.9	1198	6	Abn95676	Gene #217
24	372.2	41.8	776	6	Abk55419	Human col
25	372.2	41.8	900	6	Abk34273	Human CDN
26	372.2	41.8	938	10	ADD22487	HLA-B46 T
27	372.2	41.8	938	10	ADI15962	Human pp
28	371	41.6	593	6	Abk55034	Human col
29	369.4	41.5	456	9	Ach36218	Human end
30	367	41.2	545	6	Abk55117	Human col
31	367	41.2	550	6	Abk55144	Human col
32	361.8	40.6	654	4	Aas56386	Human CDN
33	361.8	40.6	2311	8	Acc46705	Human dit
34	361.4	40.6	566	9	Ach40217	Human foe
35	357.8	40.2	574	9	Ach42084	Human foe
36	356.6	40.0	489	9	Ach32572	Human end
37	353	39.6	847	13	Acn39288	Tumour-as
38	351.8	39.5	494	12	ADO41255	Human CDN
39	351.8	39.5	549	2	Aaq85979	Human mon
40	351.8	39.5	570	9	Ach40358	Human foe
41	351.8	39.5	626	13	Acn38870	Tumour-as
42	351.8	39.5	1053	6	Aas94801	Human DNA
43	351.8	39.5	1089	12	ADQ82747	Recombina
44	350.6	39.3	736	13	Acn38201	Tumour-as
45	350.2	39.3	552	11	ADN31064	Human H-c

## ALIGNMENTS

RESULT 1

AAAI3648

ID AAAl3648 standard; CDNA; 891 BP.

XX AAAl3648;

DT 20-JUL-2000 (first entry)

DE Human oncofoetal ferritin 1 clone T16 nucleotide sequence in Figure 7.

XX Human; oncofoetal ferritin 1; OFF1; ferritin; transplantaion;  
KW pathological pregnancy; breast cancer; cytostatic; immunosuppressive;  
KW contraceptive; abortive; nontropic; vaccine; immunisation; cancer;  
KW transplant rejection; autoimmune disease; fertilisation; diagnosis;  
KW in vitro fertilization; IVF; hepatoblastoma; Hodgkin's lymphoma;  
KW leukaemia; non-Hodgkin's lymphoma; embryonal tumour; Down's Syndrome;  
KW spontaneous abortion; miscarriage; premature contraction; toxemia;  
KW premature delivery; ss.

XX Homo sapiens.

XX WO200015788-A2.

XX 23-MAR-2000.

PF 08-SEP-1999; 99WO-IL0000485.

PR 11-SEP-1998; 98IL-00126181.

XX (GARD-) GARDINO INVESTMENT NV.

XX Moroz C;

XX WPI; 2000-271427/23.

XX DNA sequence coding for oncofetal ferritin 1 protein, useful for

immunitations against breast cancer, for enhancing fertilization rates

PT during in vitro fertilization treatment and for use as a growth factor of

PT bone-marrow progenitor cells.

XX Example 7; Fig 7; 66pp; English.

CC The present sequence represents a cDNA clone designated T16 for coding

CC oncofetal ferritin 1 (OFF1) protein. OFF1 has cytostatic,  
CC immunosuppressive, contraceptive, abortive and neutrotropic activities, and  
CC can be used as a vaccine. Compositions comprising the expression vector  
CC containing an OFF1 coding sequence, and the OFF1 protein, are useful: (a)  
CC for immunisations against cancer, especially breast cancer; (b) in the  
CC treatment of transplant rejection, autoimmune diseases, pathological  
CC pregnancies; (c) for enhancing fertilisation rates during in vitro  
CC fertilisation (IVF) treatment; and (d) for use as a growth factor of bone  
CC -marrow progenitor cells such as granulocyte monocytes. The OFF1  
CC nucleotide sequence is useful for diagnosing cancer such as breast  
CC cancer, hepatoblastoma, leukaemia, Hodgkin's and non-Hodgkin's lymphomas  
CC and embryonal tumours, Down's Syndrome, and pathological pregnancies such  
CC as spontaneous abortion and miscarriage, premature contractions, toxemia  
CC or premature delivery  
XX  
SQ Query Match 100.0%; Score 891; DB 3; Length 891;  
Best Local Similarity 100.0%; Pred. No. 6.6e-260;  
Matches 891; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGACACAGACCAACTGGTAATGTAGTAGCGCGCTGAGCTGGATTCCAAAAATG 60  
DB 1 TTGACACAGACCAACTGGTAATGTAGTAGCGCGCTGAGCTGGATTCCAAAAATG 60

QY 61 TAATGCACACTCCATTGCATTTCAGCCCGCTCTCTTAGTCGCGCCATGACGACCGCGT 120  
DB 61 TAATGCACACTCCATTGCATTTCAGCCCGCTCTCTTAGTCGCGCCATGACGACCGCGT 120

QY 121 CCACCTCGCAGGTGCGCAGAACTACCAACAGGACTCAGAGCGCGCCATCAACCGCCAGA 180  
DB 121 CCACCTCGCAGGTGCGCAGAACTACCAACAGGACTCAGAGCGCGCCATCAACCGCCAGA 180

QY 181 TCAACTGGAGCTCTACGCGCTCTACGTTTACCTGTCTTCTTACTCTTCTTACCGCG 240  
DB 181 TCAACTGGAGCTCTACGCGCTCTACGTTTACCTGTCTTCTTACTCTTCTTACCGCG 240

QY 241 ATGATGTGCTTTGAAGAACTTTGCAAAATCTTCTTCCACCAATCTCATGAGGAGGG 300  
DB 241 ATGATGTGCTTTGAAGAACTTTGCAAAATCTTCTTCCACCAATCTCATGAGGAGGG 300

QY 301 AACATGCTGAGAACTGATGAAGCTGAGAACCAACGAGGTGGCGGAATCTCTCTCAGG 360  
DB 301 AACATGCTGAGAACTGATGAAGCTGAGAACCAACGAGGTGGCGGAATCTCTCTCAGG 360

QY 361 ATATCAAGAAACACGACTGTGATGACTGGAGAGCGGCTGAATGCAATGAGTGTGCAT 420  
DB 361 ATATCAAGAAACACGACTGTGATGACTGGAGAGCGGCTGAATGCAATGAGTGTGCAT 420

QY 421 TACATTTGGAAAAAATGTGAATCAGTCACTACTGGAATTCCTTCTCTATCTCTCCA 480  
DB 421 TACATTTGGAAAAAATGTGAATCAGTCACTACTGGAATTCCTTCTCTATCTCTCCA 480

QY 481 GTCTAGCTGTGGCATCTACTACTACTAGACCGGCACTCAACACCACTTCTTC 540  
DB 481 GTCTAGCTGTGGCATCTACTACTACTAGACCGGCACTCAACACCACTTCTTC 540

QY 541 GACCCGCGGAGGAGACGCCCATTTATACCAACCTATTCTGATTTTTTCGGTCA 600  
DB 541 GACCCGCGGAGGAGACGCCCATTTATACCAACCTATTCTGATTTTTTCGGTCA 600

QY 601 CTGAAGTTTATATTCTTATCTTACAGGCTTGGAAATATCTCCATTTGTAACTTAC 660  
DB 601 CTGAAGTTTATATTCTTATCTTACAGGCTTGGAAATATCTCCATTTGTAACTTAC 660

QY 661 TACTCCGGAATCGCTGTGCTTACCTTACCTTACTGAGGCGCCCTCTCTATGAC 720  
DB 661 TACTCCGGAATCGCTGTGCTTACCTTACCTTACTGAGGCGCCCTCTCTATGAC 720

QY 721 CTAATTGGAAGGCCACCTAGCAATATCAACCATTTAACTTCCCTTACACTTATCATC 780  
DB 721 CTAATTGGAAGGCCACCTAGCAATATCAACCATTTAACTTCCCTTACACTTATCATC 780

QY 781 TTCAAAATCTTAATCTTACTGACTTCTAGAAATCGTGTGCGCTTAATCAAGCCTAC 840  
DB 781 TTCAAAATCTTAATCTTACTGACTTCTAGAAATCGTGTGCGCTTAATCAAGCCTAC 840

QY 841 GTTTTCACACTTCTAGTAAGCCTCTACTGCGAGCAACACATATAAAAAA 891  
DB 841 GTTTTCACACTTCTAGTAAGCCTCTACTGCGAGCAACACATATAAAAAA 891

RESULT 2  
AAAL3614  
ID AAAL3614 standard; cDNA; 891 BP.  
XX  
AC AAAL3614;  
XX  
DT 20-JUL-2000 (first entry)  
XX  
DE Human oncofetal ferritin 1 clone T16 nucleotide sequence in Figure 1.

XX KW Human; oncofetal ferritin 1; OFF1; ferritin; transplantation;  
XX KW pathological pregnancy; breast cancer; cytostatic; immunosuppressive;  
XX KW contraceptive; abortive; neutrotropic; vaccine; immunisation; cancer;  
XX KW transplant rejection; autoimmune disease; fertilisation; diagnosis;  
XX KW in vitro fertilization; IVF; hepatoblastoma; Hodgkin's lymphoma;  
XX KW leukaemia; non-Hodgkin's lymphoma; embryonal tumour; Down's Syndrome;  
XX KW spontaneous abortion; miscarriage; premature contraction; toxemia;  
XX KW premature delivery; ss.  
XX OS Homo sapiens.  
XX WO200015788-A2.  
XX PD 23-MAR-2000.  
XX PF 08-SEP-1999; 99WO-IL000485.  
XX PR 11-SEP-1998; 98IL-00126181.  
XX PA (GARD-) GARDINO INVESTMENT NV.  
XX PI Moroz C;  
XX WPI; 2000-271427/23.

DNA sequence coding for oncofetal ferritin 1 protein, useful for immunisations against breast cancer, for enhancing fertilization rates during in vitro fertilization treatment and for use as a growth factor of bone-marrow progenitor cells.

Claim 1; Fig 1; 66pp; English.

The present sequence represents a cDNA clone designated T16 for coding oncofetal ferritin 1 (OFF1) protein. OFF1 has cytostatic, immunosuppressive, contraceptive, abortive and neutrotropic activities, and can be used as a vaccine. Compositions comprising the expression vector containing an OFF1 coding sequence, and the OFF1 protein, are useful: (a) for immunisations against cancer, especially breast cancer; (b) in the treatment of transplant rejection, autoimmune diseases, pathological pregnancies; (c) for enhancing fertilisation rates during in vitro fertilisation (IVF) treatment; and (d) for use as a growth factor of bone marrow progenitor cells such as granulocyte monocytes. The OFF1 nucleotide sequence is useful for diagnosing cancer such as breast cancer, hepatoblastoma, leukaemia, Hodgkin's and non-Hodgkin's lymphomas and embryonal tumours, Down's Syndrome, and pathological pregnancies such as spontaneous abortion and miscarriage, premature contractions, coxaemia or premature delivery

Sequence 891 BP; 243 A; 268 C; 160 G; 220 T; 0 U; 0 Other;

Query Match 97.1%; Score 864.8; DB 3; Length 891;

Best Local Similarity 99.6%; Pred. No. 6.1e-252;

Matches 888; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

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QY 1 TTGACACAGACCAACTGGTATGTAGGACCGCGCTCAGCTGGAATTCACAAATG 60
Db 1 TTGACACAGACCAACTGGTATGTAGGACCGCGCTCAGCTGGAATTCACAAATG 59
QY 61 TAATGACACACTCCATT-GCAATTCAGCCCGCTCTCTTAGTCGCGCCATGACGACCGG 119
Db 60 TAATGACACACTCCATTGGCAATTCAGCCCGCTCTCTTAGTCGCGCCATGACGACCGG 119
QY 120 TCCACCTGCGAGGTGGCGAGAACTACACACAGGACTCAGAGGCGCCATCAACCGCCAG 179
Db 120 TCCACCTGCGAGGTGGCGAGAACTACACACAGGACTCAGAGGCGCCATCAACCGCCAG 179
QY 180 ATCAACCTGGAGCTCTAGCCCTCTACGTTTACCTGTCATGCTTACTTACTTTCACCGC 239
Db 180 ATCAACCTGGAGCTCTAGCCCTCTACGTTTACCTGTCATGCTTACTTACTTTCACCGC 239
QY 240 GATGATGTGGCTTTGAAGAACTTTGCCAAATCTTTTTCACCAATCTCATGAGGAGG 299
Db 240 GATGATGTGGCTTTGAAGAACTTTGCCAAATCTTTTTCACCAATCTCATGAGGAGG 299
QY 300 GAACTGTGAGAACTGATGAAGCTGCAGAACTCAGAGGCTGGCGGATCTTCTTCTCAG 359
Db 300 GAACTGTGAGAACTGATGAAGCTGCAGAACTCAGAGGCTGGCGGATCTTCTTCTCAG 359
QY 360 GATATCAAGAAACCACTGTCATGACTGGGAGAGCGGCTGAATGCAATGGAGTGCA 419
Db 360 GATATCAAGAAACCACTGTCATGACTGGGAGAGCGGCTGAATGCAATGGAGTGCA 419
QY 420 TTACATTTGGAAAAAATGTGAATCAGTCACTGCTGGAATTCCTTCTCTCTCTCC 479
Db 420 TTACATTTGGAAAAAATGTGAATCAGTCACTGCTGGAATTCCTTCTCTCTCTCC 479
QY 480 AGTCTAGTGTGGGACACTATATCTACTTAACAGACCGCACTCAACACCACTTCTT 539
Db 480 AGTCTAGTGTGGGACACTATATCTACTTAACAGACCGCACTCAACACCACTTCTT 539
QY 540 CGACCCCGCGGAGAGAGCCCATCTATACCAACACCTATCTGATTTTCGGTCA 599
Db 540 CGACCCCGCGGAGAGAGCCCATCTATACCAACACCTATCTGATTTTCGGTCA 599
QY 600 CCTGAAAGTTATATCTTATCTACAGGCTTCGGAATTAATCTCCCATATGTAACCTA 659
Db 600 CCTGAAAGTTATATCTTATCTACAGGCTTCGGAATTAATCTCCCATATGTAACCTA 659
QY 660 CTACTCCGGAATTCGCTGTGCTTAACCGCTTAACATTAAGCGCCACCTACTCATGCA 719
Db 660 CTACTCCGGAATTCGCTGTGCTTAACCGCTTAACATTAAGCGCCACCTACTCATGCA 719
QY 720 CCTAATTTGAGGCGCCACCTAGCAATATACCAATTAACCTTCCCTCTACACTTATCAT 779
Db 720 CCTAATTTGAGGCGCCACCTAGCAATATACCAATTAACCTTCCCTCTACACTTATCAT 779
QY 780 CTTCAAAATCTTAATTTACTGACTATCTAGAAATCGCTGCGCTTAATCCAGGCTTA 839
Db 780 CTTCAAAATCTTAATTTACTGACTATCTAGAAATCGCTGCGCTTAATCCAGGCTTA 839
QY 840 CTTTTTCACTTTCTAGTAAGCTCTTACCTGACGACACACATATAAAAAA 891
Db 840 CTTTTTCACTTTCTAGTAAGCTCTTACCTGACGACACACATATAAAAAA 891
```

## RESULT 3

AAAL13615  
ID AAAL13615 standard; cDNA; 891 BP.

AC AAAL13615;

XX 20-JUL-2000 (first entry)

DT Human oncofoetal ferritin 1 clone T16 nucleotide sequence in Figure 4.

DE Human; oncofoetal ferritin 1; OFF1; ferritin; transplacental;

XX Human; pathological pregnancy; breast cancer; cytostatic; immunosuppressive;

KW Human; pathological pregnancy; breast cancer; cytostatic; immunosuppressive;

KW contraceptive; abortive; neutropic; vaccine; immunisation; cancer;  
KW transplant rejection; autoimmune disease; fertilisation; diagnosis;  
KW in vitro fertilization; IVF; hepatoblastoma; Hodgkin's lymphoma;  
KW leukaemia; non-Hodgkin's lymphoma; embryonal tumour; Down's Syndrome;  
KW spontaneous abortion; miscarriage; premature contraction; toxemia;  
KW premature delivery; ss.

OS Homo sapiens.

XX WO200015788-A2.

XX 23-MAR-2000.

XX 08-SEP-1999; 99WO-IL000485.

XX 11-SEP-1998; 98IL-00126181.

XX (GARD-) GARDINO INVESTMENT NV.

XX Moroz C;

XX WPI; 2000-271427/23.

PT DNA sequence coding for oncofetal ferritin 1 protein, useful for  
PT immunizations against breast cancer, for enhancing fertilization rates  
PT during in vitro fertilization treatment and for use as a growth factor of  
PT bone-marrow progenitor cells.

XX Claim 1; Fig 4; 66pp; English.

CC The present sequence represents a cDNA clone designated T16 for coding  
CC oncofetal ferritin 1 (OFF1) protein. OFF1 has cytostatic,  
CC immunosuppressive, contraceptive, abortive and neutropic activities, and  
CC can be used as a vaccine. Compositions comprising the expression vector  
CC containing an OFF1 coding sequence, and the OFF1 protein, are useful: (a)  
CC for immunisations against cancer, especially breast cancer; (b) in the  
CC treatment of transplant rejection, autoimmune diseases, pathological  
CC pregnancies; (c) for enhancing fertilisation rates during in vitro  
CC fertilisation (IVF) treatment; and (d) for use as a growth factor of bone  
CC -marrow progenitor cells such as granulocyte monocytes. The OFF1  
CC nucleotide sequence is useful for diagnosing cancer such as breast  
CC cancer, hepatoblastoma, leukaemia, Hodgkin's and non-Hodgkin's lymphomas  
CC and embryonal tumours, Down's Syndrome, and pathological pregnancies such  
CC as spontaneous abortion and miscarriage, premature contractions, toxemia  
CC or premature delivery

XX Sequence 891 BP; 243 A; 266 C; 162 G; 220 T; 0 U; 0 Other;

Query Match 96.7%; Score 861.6; DB 3; Length 891;

Best Local Similarity 99.3%; Pred. No. 5.7e-251; Mismatches 4; Gaps 2;  
Matches 886; Conservative 0; Indels 2;

QY 1 TTGACACAGACCAACTGGTATGTAGGACCGCGCTCAGCTGGAATTCACAAATG 60

Db 1 TTGACACAGACCAACTGGTATGTAGGACCGCGCTCAGCTGGAATTCACAAATG 59

QY 61 TAATGACACACTCCATT-GCAATTCAGCCCGCTCTCTTAGTCGCGCCATGACGACCGG 119

Db 60 TAATGACACACTCCATTGGCAATTCAGCCCGCTCTCTTAGTCGCGCCATGACGACCGG 119

QY 120 TCCACCTGCGAGGTGGCGAGAACTACACAGGACTCAGAGGCGCCATCAACCGCCAG 179

Db 120 TCCACCTGCGAGGTGGCGAGAACTACACAGGACTCAGAGGCGCCATCAACCGCCAG 179

QY 180 ATCAACCTGGAGCTCTAGCCCTCTACGTTTACCTGTCATGCTTACTTACTTTCACCGC 239

Db 180 ATCAACCTGGAGCTCTAGCCCTCTACGTTTACCTGTCATGCTTACTTACTTTCACCGC 239

QY 240 GATGATGTGGCTTTGAAGAACTTTGCCAAATCTTTTTCACCAATCTCATGAGGAGG 299

Db 240 GATGATGTGGCTTTGAAGAACTTTGCCAAATCTTTTTCACCAATCTCATGAGGAGG 299

QY 300 GAACTGTGAGAACTGATGAAGCTGACAGGAGGCTGAGAGGCTGCGGATCTTCTTCTCAG 359

Db 300 GAACATGCTGAAACATGATGAGCTGCAGAACCAACGAGGTGGCCGAATCTTCCTCAG 359  
Qy 360 GATATCAAGAAACAGAGCTGTGATGACTGGGAGAGCGGGCTGGAATGCAATGGAGTGTGCA 419  
Db 360 GATATCAAGAAACAGAGCTGTGATGACTGGGAGAGCGGGCTGGAATGCAATGGAGTGTGCA 419  
Qy 420 TTACATTTGGAAAAAATGTAATGAGTCACTACTGGAATTCCTCTCTCTCTCTCTCTCC 479  
Db 420 TTACATTTGGAAAAAATGTAATGAGTCACTACTGGAATTCCTCTCTCTCTCTCTCTCC 479  
Qy 480 AGTCTAGCTGCTGGCATCACTATCTACTAACAAGAGCGCAACCTCAACACCACTTCTT 539  
Db 480 AGTCTAGCTGCTGGCATCACTATCTACTAACAAGAGCGCAACCTCAACACCACTTCTT 539  
Qy 540 CGACCCCGGAGGAG 599  
Db 540 CGACCCCGGAGGAG 599  
Qy 600 CCCTGAAGTTTATATCTTATCTTACCTACAGGCTTCGGAATATCTCCCATATTTGAACCTTA 659  
Db 600 CCCTGAAGTTTATATCTTATCTTACCTACAGGCTTCGGAATATCTCCCATATTTGAACCTTA 659  
Qy 660 CTACTCCGAAATCGCTGTGCTTAACCGCTAAACATTTACTGAGGCCACCTTACTCATGCA 719  
Db 660 CTACTCCGAAATCGCTGTGCTTAACCGCTAAACATTTACTGAGGCCACCTTACTCATGCA 719  
Qy 720 CTAATTTGGAAGCGGAG 779  
Db 720 CTAATTTGGAAGCGGAG 779  
Qy 780 CTTCAACATTTCTAATTTCTACTGACTATCTAGAAATCGCTGCGCTTTAAATCCAGGCTA 839  
Db 780 CTTCAACATTTCTAATTTCTACTGACTATCTAGAAATCGCTGCGCTTTAAATCCAGGCTA 839  
Qy 840 CGTTTTACACTTCTAGTAAGCTCTACTGCAAGCAACACATATAAAAAA 891  
Db 840 CGTTTTACACTTCTAGTAAGCTCTACTGCAAGCAACACATATAAAAAA 891

RESULT 4  
ID AAA13647  
XX AAA13647 standard; cDNA; 868 BP.  
AC AAA13647;  
XX  
XX  
XX 20-JUL-2000 (first entry)  
XX  
XX Human oncofoetal ferritin 1 nucleotide sequence.  
XX  
XX Human; oncofoetal ferritin 1; OFP1; ferritin; transplantation;  
XX pathological pregnancy; breast cancer; cytostatic; immunosuppressive;  
XX contraceptive; abortive; nontropic; vaccine; immunisation; cancer;  
XX transplant rejection; autoimmune disease; fertilisation; diagnosis;  
XX in vitro fertilization; IVF; hepatoblastoma; Hodgkin's lymphoma;  
XX leukaemia; non-Hodgkin's lymphoma; embryonal tumour; Down's Syndrome;  
XX spontaneous abortion; miscarriage; premature contraction; toxemia;  
XX premature delivery; ss.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX 108..605  
XX CDS /tag= a  
XX FT /product= "oncofoetal ferritin 1"  
XX FT  
XX  
XX WO200015788-A2.  
XX  
XX 23-MAR-2000.  
XX  
XX 08-SEP-1999; 99WO-IL000485.  
XX  
XX 11-SEP-1998; 98IL-00126181.  
XX  
XX PR

XX  
PA  
XX  
XX (GARD-) GARDINO INVESTMENT NV.  
PI Moroz C;  
XX  
XX WPI; 2000-271427/23.  
DR P-PSDB; AAY53271.  
XX  
XX DNA sequence coding for oncofetal ferritin 1 protein, useful for  
PT immunizations against breast cancer, for enhancing fertilization rates  
PT during in vitro fertilization treatment and for use as a growth factor of  
PT bone-marrow progenitor cells.  
XX  
XX Example 7; Fig 5; 66pp; English.  
XX  
XX The present sequence encodes the human oncofetal ferritin 1 (OFP1)  
CC protein. OFP1 has cytostatic, immunosuppressive, contraceptive, abortive  
CC and nontropic activities, and can be used as a vaccine. Compositions  
CC comprising the expression vector containing an OFP1 coding sequence, and  
CC the OFP1 protein, are useful: (a) for immunisations against cancer,  
CC especially breast cancer; (b) in the treatment of transplant rejections,  
CC autoimmune diseases, pathological pregnancies; (c) for enhancing  
CC fertilisation rates during in vitro fertilisation (IVF) treatment; and  
CC (d) for use as a growth factor of bone-marrow progenitor cells such as  
CC granulocyte monocytes. The OFP1 nucleotide sequence is useful for  
CC diagnosing cancer such as breast cancer, hepatoblastoma, leukaemia,  
CC Hodgkin's and non-Hodgkin's lymphomas and embryonal tumours, Down's  
CC Syndrome, and pathological pregnancies such as spontaneous abortion and  
CC miscarriage, premature contractions, toxemia or premature delivery  
XX  
XX Sequence 868 BP; 237 A; 260 C; 156 G; 215 T; 0 U; 0 Other;  
SQ

Query Match 95.6%; Score 852; DB 3; Length 868;  
Best Local Similarity 100.0%; Pred. No. 4.7e-248;  
Matches 852; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTGACACAGACCACTGGTAATGGTAGCGACGGGCTCAGCTGGAAATTCGAAAAATG 60  
Db 1 TTGACACAGACCACTGGTAATGGTAGCGACGGGCTCAGCTGGAAATTCGAAAAATG 60  
Qy 61 TAATGACACTCCATTCGATTCAGCGCGCTCTCTTAGTCGCGCCATGACGACCGCGT 120  
Db 61 TAATGACACTCCATTCGATTCAGCGCGCTCTCTTAGTCGCGCCATGACGACCGCGT 120  
Qy 121 CCACCTCGAGGTGGCGCCAGAACTACACAGGACTCAGAGGCGCCATCAACCGCCAGA 180  
Db 121 CCACCTCGAGGTGGCGCCAGAACTACACAGGACTCAGAGGCGCCATCAACCGCCAGA 180  
Qy 181 TCAACCTGGAGCTCTACGCTCTCTACGTTTACCTGTCATGCTTACTTTCACCGCG 240  
Db 181 TCAACCTGGAGCTCTACGCTCTCTACGTTTACCTGTCATGCTTACTTTCACCGCG 240  
Qy 241 ATGATGCTGCTTTCAAGAACTTTGCCAAATACTTTCTTCCAAATCTCATGAGGAGGG 300  
Db 241 ATGATGCTGCTTTCAAGAACTTTGCCAAATACTTTCTTCCAAATCTCATGAGGAGGG 300  
Qy 301 AACATGCTGAGAACTGATGAAGTGCAGAACCAACAGAGTGGCGGAATCTTCTTCAGG 360  
Db 301 AACATGCTGAGAACTGATGAAGTGCAGAACCAACAGAGTGGCGGAATCTTCTTCAGG 360  
Qy 361 ATATCAAGAACCACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
Db 361 ATATCAAGAACCACTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
Qy 421 TACATTTGGAAAAAATGTAATGAGTCACTACTGGAATTCCTCTCTCTCTCTCTCC 480  
Db 421 TACATTTGGAAAAAATGTAATGAGTCACTACTGGAATTCCTCTCTCTCTCTCTCC 480  
Qy 481 GTCTTAGCTGCTGGCATCACTATCTACTAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
Db 481 GTCTTAGCTGCTGGCATCACTATCTACTAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
Qy 541 GACCCCGGAGGAG 600  
Db 541 GACCCCGGAGGAG 600





[illegible]



XX 22-JUL-2004.  
 XX 15-OCT-2003; 2003WO-US029126.  
 XX 18-OCT-2002; 2002US-0419988P.  
 XX (GETH ) GENENTECH INC.  
 PA (WUTD/) WU T D.  
 PA (ZHOU/) ZHOU Y.  
 PI Wu TD, Zhou Y;  
 XX WPI; 2004-534300/51.  
 XX New nucleic acid molecule and encoded polypeptide, for diagnosing,  
 PT preventing or treating cell proliferative disorders such as cancer.  
 XX Claim 1; SEQ ID NO 2032; 5504pp; English.  
 XX  
 XX The present invention describes an isolated tumour-associated antigenic  
 CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide  
 CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of  
 CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%  
 CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-  
 CC (c). Also described: (1) an expression vector comprising the above  
 CC nucleic acid; (2) a host cell comprising the above expression vector; (3)  
 CC a process for producing a polypeptide; (4) an isolated polypeptide  
 CC comprising: (a) an amino acid sequence encoded by any of the above  
 CC nucleotide sequences; (b) an amino acid sequence encoded by the full-  
 CC length coding region of the above nucleotide sequences; or (c) a sequence  
 CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide  
 CC comprising the above polypeptide fused to a heterologous polypeptide; (6)  
 CC an isolated antibody that binds to the above polypeptide; (7) a process  
 CC for producing the antibody; (8) an isolated oligopeptide that binds to  
 CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)  
 CC binding organic molecule that binds to the above polypeptide; (10) a  
 CC composition of matter comprising the above (chimeric) polypeptide,  
 CC antibody, oligopeptide or TAT binding organic molecule, in combination  
 CC with a carrier; (11) an article of manufacture comprising a container and  
 CC the composition of matter contained within the container; (12) methods of  
 CC inhibiting the growth of a cell that expresses the above protein, where  
 CC the growth of the cell is at least in part dependent upon a growth  
 CC potentiating effect of the above protein; (13) a method of  
 CC therapeutically treating a mammal having a cancerous tumour comprising  
 CC cells that express the above protein; (14) a method of determining the  
 CC presence of a protein in a sample suspected of containing the protein  
 CC described above; (15) methods of diagnosing the presence of a tumour in a  
 CC mammal; (16) a method for treating or preventing a cell proliferative  
 CC disorder associated with increased expression or activity of the above  
 CC protein; and (17) a method of binding an antibody, oligopeptide or  
 CC organic molecule to a cell that expresses the protein described above.  
 CC The TAT sequences have cytostatic activities, and can be used in gene  
 CC therapy. The composition and methods are useful for diagnosing,  
 CC preventing or treating cancer. The composition is also used for preparing  
 CC a medicament for the therapeutic treatment or diagnostic detection of a  
 CC cell proliferative disorder or cancer. The present sequence represents a  
 CC human TAT cDNA sequence from the present invention.  
 XX Sequence 630 BP; 161 A; 180 C; 162 G; 127 T; 0 U; 0 Other;

Query Match 42.0%; Score 373.8; DB 13; Length 630;  
 Best Local Similarity 99.5%; Pred. No. 9.8e-103;  
 Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 86 CGGCTCTCTTACGCGGCGCATACGACCGGCTCCACCTCGAGGTCGCCAGACTA 145  
 DB 40 CGGCTCTCTTACGCGGCGCATACGACCGGCTCCACCTCGAGGTCGCCAGACTA 99  
 QY 146 CCACGAGACTCAGAGCGGCGCATACGACCGGCGCATACGACCTGAGCTCTAGCCTCCTA 205  
 DB 100 CCACGAGACTCAGAGCGGCGCATACGACCGGCGCATACGACCTGAGCTCTAGCCTCCTA 159

QY 206 CGTTTACCTGTCCATGTCTTACTACTTTGACCGCGATGATGTGGCTTTGAAGAACTTTGC 265  
 DB 160 CGTTTACCTGTCCATGTCTTACTACTTTGACCGCGATGATGTGGCTTTGAAGAACTTTGC 219  
 QY 266 CAAATACCTTCTTCCCAATCTCATGAGGAGGAGGACATGCTGAGAACTGNTGAAGCT 325  
 DB 220 CAAATACCTTCTTCCCAATCTCATGAGGAGGAGGAGGAAATGCTGAGAACTGNTGAAGCT 279  
 QY 326 GCAGAACCAACGAGGTGGCCGAATCTTCTTCCAGGATATCAAGAAACACAGACTGTGATGA 385  
 DB 280 GCAGAACCAACGAGGTGGCCGAATCTTCTTCCAGGATATCAAGAAACACAGACTGTGATGA 339  
 QY 386 CTGGGAGAGCGGCTGAATGCAATGGAGTGTGCATTCATTTGGAAAAAATGGAATCA 445  
 DB 340 CTGGGAGAGCGGCTGAATGCAATGGAGTGTGCATTCATTTGGAAAAAATGGAATCA 399  
 QY 446 GTCACTACTGCAATTC 462  
 DB 400 GTCACCTACTGGAAGTGC 416  
 RESULT 10  
 ACN39230  
 ID ACN39230 standard; cDNA; 630 BP.  
 XX ACN39230;  
 AC ACN39230;  
 DT 18-NOV-2004 (first entry)  
 XX Tumour-associated antigenic target (TAT) cDNA DNA325475, SEQ ID NO:3247.  
 DE Tumour-associated antigenic target; TAT; human; overexpression; cancer;  
 XX tumour; diagnosis; cell proliferative disorder; breast cancer;  
 KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;  
 KW central nervous system cancer; bladder cancer; pancreatic cancer;  
 KW cervical cancer; melanoma; leukaemia; hybridisation probe;  
 KW chromosome identification; chromosome mapping; gene mapping;  
 KW gene therapy; cytostatic; gene; ss.  
 XX Homo sapiens.  
 OS WO2004030615-A2.  
 PN 15-APR-2004.  
 PD 29-SEP-2003; 2003WO-US028547.  
 PF 02-OCT-2002; 2002US-0414971P.  
 XX (GETH ) GENENTECH INC.  
 XX Wu TD, Zhang Z, Zhou Y;  
 XX WPI; 2004-347921/32.  
 XX New tumor-associated antigenic target polypeptides and nucleic acids,  
 PT useful in preparing a medicament for treating or detecting a  
 PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or  
 PT prostate cancer or tumor.  
 XX Claim 1; SEQ ID NO 3247; 7273pp; English.  
 PS The invention relates to human tumour-associated antigenic target (TAT)  
 CC polypeptides, and their related nucleic acids. The TAT polypeptides are  
 CC overexpressed in cancer tissues compared to normal tissues, and may thus  
 CC serve as effective targets for the diagnosis and treatment of cancer in  
 CC mammals. The invention also relates to the TAT nucleic acids and  
 CC sequences at least 80% identical to the TAT nucleic acids and  
 CC polypeptides; expression vectors and host cells comprising a TAT nucleic  
 CC acid; an antibody specific for a TAT polypeptide; a peptide or organic  
 CC molecule which binds to a TAT polypeptide; fusion proteins comprising a  
 CC TAT polypeptide; and methods and compositions for the treatment or  
 CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,

CC antibodies, antagonists, binding molecules and compositions are useful  
CC for diagnosing or treating a cell proliferative disorder associated with  
CC increased TAT expression, particularly cancers such as breast cancer,  
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder  
CC cancer, pancreatic cancer, cervical cancer, cancers of the central  
CC nervous system, melanoma and leukemia. TAT nucleic acids may further be  
CC used as hybridisation probes, in chromosome and gene mapping, in  
CC chromosome identification and in gene therapy. The present sequence  
CC represents a TAT nucleic acid of the invention

XX  
SQ Sequence 630 BP; 161 A; 180 C; 162 G; 127 T; 0 U; 0 Other;

Query Match 42.0%; Score 373.8; DB 13; Length 630;  
Best Local Similarity 99.5%; Pred. No. 9.8e-103;  
Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 86 CCGCTCTCTTCTAGTGGCGCCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGAACTA 145  
DB 40 CCGCTCTCTTCTAGTGGCGCCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGAACTA 99  
QY 146 CCACGAGACTCAGAGCGCGCCATCAACCGCCAGATCAACCTGGAGCTCTAGCCTCCTA 205  
DB 100 CCACGAGACTCAGAGCGCGCCATCAACCGCCAGATCAACCTGGAGCTCTAGCCTCCTA 159  
QY 206 CTTTTACCTGTCATGTCTTACTTCTTGACCGCGATGATGGCTTTGAAGAACTTTGC 265  
DB 160 CTTTTACCTGTCATGTCTTACTTCTTGACCGCGATGATGGCTTTGAAGAACTTTGC 219  
QY 266 CAAATACCTTTCTTCCACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 325  
DB 220 CAAATACCTTTCTTCCACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 279  
QY 326 CGAGAACCAACGAGTGGCGGAATCTTCTTCCAGGATATCAAGAACCGAGCTGTGATGA 385  
DB 280 CGAGAACCAACGAGTGGCGGAATCTTCTTCCAGGATATCAAGAACCGAGCTGTGATGA 339  
QY 386 CTGGGAGAGCGGCTGAATGCAATGGAGTGCATTACATTTGGAAGAAATGTGAATCA 445  
DB 340 CTGGGAGAGCGGCTGAATGCAATGGAGTGCATTACATTTGGAAGAAATGTGAATCA 399  
QY 446 GTCACTACTGGAATTC 462  
DB 400 GTCACTACTGGAATTC 416

## RESULT 11

AAH02927

ID AAH02927 standard; DNA; 790 BP.

XX  
XX  
AC AAH02927;

DT 15-JUN-2001 (first entry)

DE Human shear stress-response coding sequence SEQ ID NO: 107.

KW Human; shear stress-response protein; vascular disease; arteriosclerosis;  
KW ds.

XX Homo sapiens.

XX WO200125427-A1.

XX 12-APR-2001.

XX 02-OCT-2000; 2000WO-JP006840.

XX 01-OCT-1999; 99JP-00280976.

XX (KYOW ) KYOWA HAKKO KOGYO KK.

XX (NOJI/) NOJIMA H.

PI Nojima H, Yoshie H, Obayashi M, Ota T, Kawabata A, Sakurada K;

PI Kuga T, Sekine S, Nakamura Y, Sugano S;

XX  
DR

WPI; 2001-266308/27.

P-PSDB; AAB90804.

XX DNA sequences, proteins encoded by them and antibodies against them  
PT useful in diagnosis and treatment of vascular disease caused by  
PT arteriosclerosis.

XX Claim 20; Page 537-539; 678pp; Japanese.

XX The present invention provides the protein and coding sequences of a  
CC number of human shear stress response proteins. These are useful in the  
CC diagnosis, treatment and screening of vascular diseases caused by  
CC arteriosclerosis, including heart failure, post-PTCA restenosis and  
CC hypertension

XX Sequence 790 BP; 207 A; 221 C; 184 G; 178 T; 0 U; 0 Other;

Query Match 42.0%; Score 373.8; DB 4; Length 790;  
Best Local Similarity 99.5%; Pred. No. 1.1e-102;  
Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 86 CCGCTCTCTTCTAGTGGCGCCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGAACTA 145  
DB 56 CCGCTCTCTTCTAGTGGCGCCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGAACTA 115  
QY 146 CCACGAGACTCAGAGCGCGCCATCAACCGCCAGATCAACCTGGAGCTCTAGCCTCCTA 205  
DB 116 CCACGAGACTCAGAGCGCGCCATCAACCGCCAGATCAACCTGGAGCTCTAGCCTCCTA 175  
QY 206 CTTTTACCTGTCATGTCTTACTTCTTGACCGCGATGATGGCTTTGAAGAACTTTGC 265  
DB 176 CTTTTACCTGTCATGTCTTACTTCTTGACCGCGATGATGGCTTTGAAGAACTTTGC 235  
QY 266 CAAATACCTTTCTTCCACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 325  
DB 236 CAAATACCTTTCTTCCACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 295  
QY 326 CGAGAACCAACGAGTGGCGGAATCTTCTTCCAGGATATCAAGAACCGAGCTGTGATGA 385  
DB 296 CGAGAACCAACGAGTGGCGGAATCTTCTTCCAGGATATCAAGAACCGAGCTGTGATGA 355  
QY 386 CTGGGAGAGCGGCTGAATGCAATGGAGTGCATTACATTTGGAAGAAATGTGAATCA 445  
DB 356 CTGGGAGAGCGGCTGAATGCAATGGAGTGCATTACATTTGGAAGAAATGTGAATCA 415  
QY 446 GTCACTACTGGAATTC 462  
DB 416 GTCACTACTGGAATTC 432

## RESULT 12

ADQ29634

ID ADQ29634 standard; DNA; 801 BP.

XX  
AC ADQ29634;

DT 07-OCT-2004 (first entry)

DE Human colorectal cancer-associated protein coding sequence #56.

XX human; colon cancer; TIMP1; Reg1-alpha;

KW colorectal cancer-associated marker; gene; ds.

XX Homo sapiens.

XX EP1439393-A2.

XX 21-JUL-2004.

XX 15-DEC-2003; 2003EP-00257868.

XX 13-DEC-2002; 2002US-0433554P.

PR 31-JUL-2003; 2003US-0491397P.  
XX (FARB ) BAYER HEALTHCARE LLC.  
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
XX  
PI Astle JH, Boardman LA, Bugart LJ, Burgess CC, Catino TJ;  
PI Dwivedi P, Huntress M, Johnson KA, Lewis ME, Maimonis PJ, Myerow SH;  
PI Brown-Shimer SLA, Thiagalingam A, Thibodeau SN, Molino GA;  
XX  
XX WPI; 2004-545561/53.  
DR P-PSDB; ADQ29701.  
DR  
XX  
XX Diagnosing colon cancer in individual, preferably human, by detecting  
PT presence of TIMP 1 in sample, where presence of TIMP 1 in sample is  
PT indicative of colon cancer in individual.  
XX  
XX Claim 7; SEQ ID NO 60; 433pp; English.  
XX  
XX The invention comprises a method for diagnosing colon cancer in an  
CC individual, the method involves obtaining a serum sample from the  
CC individual and detecting the presence of either TIMP1 or Regl-alpha and  
CC an additional colorectal cancer-associated marker. The method of the  
CC invention is useful for diagnosing colon cancer in an individual. The  
CC present DNA sequence represents a human colorectal cancer-associated  
CC protein coding sequence of the invention.  
XX  
SQ Sequence 801 BP; 209 A; 226 C; 187 G; 179 T; 0 U; 0 Other;  
Query Match 42.0%; Score 373.8; DB 12; Length 801;  
Best Local Similarity 99.5%; Pred. No. 1.1e-102;  
Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 86 CGGCTCTCTTGTAGTGGCGGCGCATGACGACGCGCTCCACCTCGCAGGTGGCGCAGAACTA 145  
DB 70 CGGCTCTCTTGTAGTGGCGGCGCATGACGACGCGCTCCACCTCGCAGGTGGCGCAGAACTA 129  
QY 146 CCACGAGACTCAGAGGCGCGCATCAACCGCAGATCAACCTGGAGCTCTTACGCTCTCTA 205  
DB 130 CCACGAGACTCAGAGGCGCGCATCAACCGCAGATCAACCTGGAGCTCTTACGCTCTCTA 189  
QY 206 CGTTTACCTGCTTCTTACTACTTGTGCGGCGATGATGCTTGTGAAGAACTTTGC 265  
DB 190 GTTTTACCTGCTTCTTACTACTTGTGCGGCGATGATGCTTGTGAAGAACTTTGC 249  
QY 266 CAATATCTTCTTCAACCAATCTCATGAGGAGGGAACATGCTGAGAACTGTGAAGCT 325  
DB 250 CAATATCTTCTTCAACCAATCTCATGAGGAGGGAACATGCTGAGAACTGTGAAGCT 309  
QY 326 GCAGAACCAACGAGTGGCGGAATCTTCTTCAAGATATCAAGAAACAGACTGTGATGA 385  
DB 310 GCAGAACCAACGAGTGGCGGAATCTTCTTCAAGATATCAAGAAACAGACTGTGATGA 369  
QY 386 CTGGGAGAGCGGCTGAATGCAATGAGTGTGCATTACATTTGGAAAAATGTGAATCA 445  
DB 370 CTGGGAGAGCGGCTGAATGCAATGAGTGTGCATTACATTTGGAAAAATGTGAATCA 429  
QY 446 GTCACTACTGGAATTC 462  
DB 430 GTCACTACTGGAATTC 446  
RESULT 13  
ADP24690  
ID ADP24690 standard; cDNA; 801 BP.  
XX  
XX AC ADP24690;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE PRO polypeptide encoding cDNA SEQ ID NO:1868.  
XX  
XX ss; gene; PRO; antiinflammatory; antiarthritic; antirheumatic;  
KW immunosuppressive; osteopathic; antidiabetic; dermatological;

KW antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory;  
XX gene therapy; immune system.  
XX Unidentified.  
OS  
XX WO2004041170-A2.  
PD 21-MAY-2004.  
XX  
XX 30-OCT-2003; 2003WO-US034312.  
XX  
XX 01-NOV-2002; 2002US-0423394P.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;  
PI Wu TD;  
XX  
XX WPI; 2004-419628/39.  
DR P-PSDB; ADP24691.  
XX  
XX New PRO polypeptides and polynucleotides, useful for treating e.g.  
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated  
PT renal disease, or demyelinating diseases of the central or peripheral  
PT nervous system.  
XX  
XX Claim 1; SEQ ID NO 1868; 2940pp; English.  
XX  
XX The invention relates to a novel isolated nucleic acid and the PRO  
CC polypeptide encoded by it. A protein of the invention has  
CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,  
CC osteopathic, antidiabetic, dermatologic, antipsoriatic, antiallergic,  
CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide  
CC of the invention may have a use in gene therapy. The PRO polypeptide, its  
CC agonist, antagonist, or antibody that specifically binds to the  
CC polypeptide is useful for treating an immune related disorder such as  
CC systemic lupus erythematous, rheumatoid arthritis, osteoarthritis,  
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an  
CC idiopathic inflammatory myopathy. Sjogren's syndrome, systemic  
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal  
CC disease, a demyelinating disease of the central or peripheral nervous  
CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,  
CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary  
CC disease, infectious or autoimmune chronic active hepatitis, primary  
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,  
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's  
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin  
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic  
CC disease, asthma, allergic rhinitis, atopic dermatitis, food  
CC hypersensitivity, urticaria, an immunologic disease of the lung,  
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity  
CC pneumonitis, a transplantation associated disease, graft rejection or  
CC graft-versus-host disease. The present sequence encodes a PRO protein of  
XX the invention.  
SQ Sequence 801 BP; 209 A; 226 C; 187 G; 179 T; 0 U; 0 Other;

Query Match 42.0%; Score 373.8; DB 13; Length 801;  
Best Local Similarity 99.5%; Pred. No. 1.1e-102;  
Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 86 CGGCTCTCTTGTAGTGGCGGCGCATGACGACGCGCTCCACCTCGCAGGTGGCGCAGAACTA 145  
DB 70 CGGCTCTCTTGTAGTGGCGGCGCATGACGACGCGCTCCACCTCGCAGGTGGCGCAGAACTA 129  
QY 146 CCACGAGACTCAGAGGCGCGCATCAACCGCAGATCAACCTGGAGCTCTTACGCTCTCTA 205  
DB 130 CCACGAGACTCAGAGGCGCGCATCAACCGCAGATCAACCTGGAGCTCTTACGCTCTCTA 189  
QY 206 CGTTTACCTGCTTCTTACTACTTGTGCGGCGATGATGCTTGTGAAGAACTTTGC 265  
DB 190 GTTTTACCTGCTTCTTACTACTTGTGCGGCGATGATGCTTGTGAAGAACTTTGC 249

QY 266 CAATATCTTTCTTACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 325  
DB 250 CAATATCTTTCTTACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 309  
QY 326 CGAGAACCAACGAGGTGGCCGAATCTTCTTCAGGATATCAAGAAACAGAGCTGTGATGA 385  
DB 310 CGAGAACCAACGAGGTGGCCGAATCTTCTTCAGGATATCAAGAAACAGAGCTGTGATGA 369  
QY 386 CTGGGAGAGCGGGCTGAATGCAATGAGGTGTCATTAATTTGGAAAAAATGTGAATCA 445  
DB 370 CTGGGAGAGCGGGCTGAATGCAATGAGGTGTCATTAATTTGGAAAAAATGTGAATCA 429  
QY 446 GTCACACTGGAATTC 462  
DB 430 GTCACACTGGAATTC 446

## RESULT 14

ACN88431

ID ACN88431 standard; DNA; 830 BP.

XX AC

XX ACN88431;

DT 02-DEC-2004 (first entry)

XX Breast cancer related marker, seq id 9581.

DE Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.

XX Homo sapiens.

XX US2003099974-A1.

XX 29-MAY-2003.

XX 18-JUL-2002; 2002US-00198846.

XX 18-JUL-2001; 2001US-0306220P.

XX (MILL-) MILLENNIUM PHARM INC.

PI Lillie J, Xu Y, Wang Y, Steinmann K;

WPI; 2003-787014/74.

Novel isolated polypeptide associated with breast cancer, useful for detecting presence of polypeptide in sample, as a marker for breast cancer.

PS Disclosure; SEQ ID NO 9581; 36pp; English.

The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (S1). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for detecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACN78851-ACN92934 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web site at [seqdata.uspto.gov/sequence.html?docID=20030099974](http://seqdata.uspto.gov/sequence.html?docID=20030099974)

SQ Sequence 830 BP; 209 A; 224 C; 210 G; 184 T; 0 U; 3 Other;

## Query Match

Best Local Similarity 99.5%; Pred. No. 1.1e-102; Length 830;

Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 86 CCGCTCTCTTACTGCGCGCCATGACGACCGGCTCCACTGCGAGGTGCGCAGAACTA 145

|||||

DB 56 CCGCTCTCTTACTGCGCGCCATGACGACCGGCTCCACTGCGAGGTGCGCAGAACTA 115  
QY 146 CCACGAGACTCAGAGCGCGCCATCAACCGCCAGATCAACCTGGAGCTCTAGCGCTCCTA 205  
DB 116 CCACGAGACTCAGAGCGCGCCATCAACCGCCAGATCAACCTGGAGCTCTAGCGCTCCTA 175  
QY 206 CGTTTACTCTGCCATGCTTACTACTTTGACCGCGATGATGGCTTTGAAGAACTTTGC 265  
DB 176 CGTTTACTCTGCCATGCTTACTACTTTGACCGCGATGATGGCTTTGAAGAACTTTGC 235  
QY 266 CAATATCTTTCTTACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 325  
DB 236 CAATATCTTTCTTACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 295  
QY 326 GCAGAACCAACGAGGTGGCCGAATCTTCTTCAGGATATCAAGAAACAGAGCTGTGATGA 385  
DB 296 GCAGAACCAACGAGGTGGCCGAATCTTCTTCAGGATATCAAGAAACAGAGCTGTGATGA 355  
QY 386 CTGGGAGAGCGGGCTGAATGCAATGAGGTGTCATTAATTTGGAAAAAATGTGAATCA 445  
DB 356 CTGGGAGAGCGGGCTGAATGCAATGAGGTGTCATTAATTTGGAAAAAATGTGAATCA 415  
QY 446 GTCACACTGGAATTC 462  
DB 416 GTCACACTGGAATTC 432

## RESULT 15

AAH23073

ID AAH23073 standard; DNA; 920 BP.

XX AC

XX AAH23073;

XX 17-SEP-2001 (first entry)

XX Osteoarthritis tissue-derived nucleic acid sequence #3.

XX Osteoarthritis; infectious disorder; Crohn's disease; sepsis; human;  
wound healing; osteopathic; anti-arthritis; anti-inflammatory; vulnery;

XX antibacterial; antiallergic; ds.

XX Homo sapiens.

XX WO200153531-A2.

XX 26-JUL-2001.

XX 18-JAN-2001; 2001WO-US000016.

XX 18-JAN-2000; 2000US-0176523P.

XX (PHAA ) PHARMACIA CORP.

XX Phippard D, Vasanthakamur G, Dotson S, Ma X;

XX WPI; 2001-451914/48.

Substantially purified protein, polypeptide or their fragments, used to identify a biologically active compound or composition and treat

mammalian osteoarthritis.

XX Claim 1; Page 91-92; 144pp; English.

Sequences AAH23071-23152 represent nucleic acid sequences derived from osteoarthritis tissues. The sequences are useful as probes and for the diagnosis or prognosis of mammalian osteoarthritis. The polynucleotides and polypeptides of the invention are useful for generating diagnostic reagents, as targets for small molecule drug development, generation of therapeutics, and cloning genes. Specific antibodies are used to generate enzyme linked immunosorbent assays for detection of osteoarthritis. The invented molecules can be used to treat osteoarthritis or to analyse the disease-modifying activity of osteoarthritis drugs. Other disorders treatable using the nucleic acid sequences include atopic, inflammatory



CC and infectious disorders e.g. Crohn's disease and sepsis, and wound  
CC healing

XX

SQ Sequence 920 BP; 233 A; 272 C; 216 G; 199 T; 0 U; 0 Other;

Query Match 42.0%; Score 373.8; DB 4; Length 920;  
Best Local Similarity 99.5%; Pred.No. 1.2e-102;  
Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	86	CGCCCTCTCCTTAGTCGGCGCCATGACGACGCGTCCACCTCGCAGGTGCGCCAGAACTA	145
Db	173	CGCCCTCTCCTTAGTCGGCGCCATGACGACGCGTCCACCTCGCAGGTGCGCCAGAACTA	232
QY	146	CCACCAGGACTCAGAGGCGCCATCAACCGCCAGATCAACCTGGAGCTCTAGCCTCCTA	205
Db	233	CCACCAGGACTCAGAGGCGCCATCAACCGCCAGATCAACCTGGAGCTCTAGCCTCCTA	292
QY	206	CGTTTACCTGTCCATGCTTACTACTTTGACCGCGATGATGGCTTTGAAGAACTTTGC	265
Db	293	CGTTTACCTGTCCATGCTTACTACTTTGACCGCGATGATGGCTTTGAAGAACTTTGC	352
QY	266	CAATATCTTTCTTACCCTCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT	325
Db	353	CAATATCTTTCTTACCCTCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT	412
QY	326	GCAGAACCAACGAGGTGGCCGAATCTTCTTCAGGATATCAAGAACCCAGACTGTGATGA	385
Db	413	GCAGAACCAACGAGGTGGCCGAATCTTCTTCAGGATATCAAGAACCCAGACTGTGATGA	472
QY	386	CTGGGAGAGCGGGCTGAATGCAATGGAGTGTGCATTACATTGGAAAAAATGTGAATCA	445
Db	473	CTGGGAGAGCGGGCTGAATGCAATGGAGTGTGCATTACATTGGAAAAAATGTGAATCA	532
QY	446	GTCCTACTCTGGAATTC	462
Db	533	GTCCTACTCTGGAATTC	549

Search completed: April 1, 2005, 11:40:54  
Job time : 409 secs

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OM nucleic - nucleic search, using sw model

Run on: April 1, 2005, 11:28:57 ; Search time 141 Seconds  
(without alignments)  
10339.876 Million cell updates/sec

Title: US-09-786-867C-1  
Perfect score: 891  
Sequence: 1 ttgacaccagaccactgggt.....acgacaacacataaaaaa 891

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:  
1: /cgn2\_6/ptodata/1/ina/5A COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PTCUT COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	373.8	42.0	1462	4	US-09-949-016-4902
2	350	39.3	491	3	US-09-643-597-307
3	350	39.3	491	4	US-09-480-884A-307
4	350	39.3	491	4	US-09-542-615A-307
5	350	39.3	491	4	US-09-606-421B-307
6	350	39.3	491	4	US-09-630-940B-307
7	348.6	39.1	924	4	US-09-919-172-94
8	348.6	39.1	924	4	US-09-976-594-1076
9	341.8	38.4	9364	4	US-09-949-016-14890
10	309.6	34.7	933	4	US-09-799-451-404
11	293	32.9	32065	4	US-09-949-016-12136
12	293	32.9	32066	4	US-09-949-016-13268
13	237.2	26.6	292	4	US-09-313-294A-6635
14	225.4	25.3	601	4	US-09-949-016-115137
15	222	24.9	396	4	US-09-640-173-7
16	222	24.9	396	4	US-09-713-550-7
17	222	24.9	396	4	US-09-825-294-7
18	222	24.9	396	4	US-09-970-966-7
19	215	24.1	506	4	US-09-621-976-542
20	213.2	23.9	440	3	US-09-397-787-328
21	211.4	23.7	396	4	US-09-640-173-64
22	211.4	23.7	396	4	US-09-713-550-64
23	211.4	23.7	396	4	US-09-825-294-64
24	211.4	23.7	396	4	US-09-970-966-64
25	207.4	23.3	1613	1	US-08-219-842-1
26	207.4	23.3	1613	1	US-08-451-096-1
27	207.4	23.3	1613	2	US-08-810-599-1

28	207.4	23.3	1735	3	US-08-413-740A-1	Sequence 1, Appli
29	207.4	23.3	1735	5	PCT-US95-04063-1	Sequence 1, Appli
30	207.4	23.3	16568	4	US-09-525-906-1	Sequence 1, Appli
31	207.4	23.3	16569	3	US-09-097-889-2	Sequence 2, Appli
32	207.4	23.3	16569	3	US-09-377-856-1	Sequence 1, Appli
33	207.4	23.3	16569	3	US-09-302-681-2	Sequence 2, Appli
34	207.4	23.3	16569	4	US-09-098-079-2	Sequence 2, Appli
35	207.4	23.3	16569	4	US-10-053-611-1	Sequence 1, Appli
36	205.8	23.1	1539	4	US-09-377-497-3	Sequence 3, Appli
37	205	23.0	366	4	US-09-401-064-338	Sequence 338, App
38	204.2	22.9	6744	3	US-09-098-079-1	Sequence 1, Appli
39	204.2	22.9	6744	4	US-09-098-079-1	Sequence 1, Appli
40	201	22.6	6691	3	US-09-302-681-3	Sequence 3, Appli
41	200.6	22.5	601	4	US-09-949-016-91636	Sequence 91636, A
42	199.4	22.4	112623	4	US-09-949-016-14374	Sequence 14374, A
43	169.8	19.1	241	4	US-09-389-681-332	Sequence 332, App
44	169.8	19.1	241	4	US-09-620-405B-332	Sequence 332, App
45	169.8	19.1	241	4	US-09-433-826B-332	Sequence 332, App

## ALIGNMENTS

## RESULT 1

US-09-949-016-4902  
; Sequence 4902, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4902  
; LENGTH: 1462  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-4902

Query Match	42.0%	Score	373.8;	DB	4;	Length	1462;
Best Local Similarity	99.5%	Pred. No.	1.6e-107;				
Mismatches	375;	Conservative	0;	Mismatches	2;	Indels	0;
Gaps	0;						
QY	86	CGCGCTCTCTTAGTCGCGCGCATGACGACCGCGTCCACCTCGCAGGTGCGCGCAACTA	145				
Db	187	CGCGCTCTCTTAGTCGCGCGCATGACGACCGCGTCCACCTCGCAGGTGCGCGCAACTA	246				
QY	146	CCACGAGACTCAGAGCGCGCATCAACCGCAGATCAACCTGGAGCTCTACGCTCTCTA	205				
Db	247	CCACGAGACTCAGAGCGCGCATCAACCGCAGATCAACCTGGAGCTCTACGCTCTCTA	306				
QY	206	CGTTTACCTGTCATGCTTACTACTTACTTACCGCGCATGATGGCTTTGAAGAACTTTGC	265				
Db	307	CGTTTACCTGTCATGCTTACTACTTACTTACCGCGCATGATGGCTTTGAAGAACTTTGC	366				
QY	266	CAATATCTTCTTCCCAATCTCATGAGGAGGGAACATCTGAGAACTGATGAAGCT	325				
Db	367	CAATATCTTCTTCCCAATCTCATGAGGAGGGAACATCTGAGAACTGATGAAGCT	426				
QY	326	GCAGAACCAACGAGGTGGCCGAATCTTCTTCAAGATATCAAGAACACAGACTGTGATGA	385				
Db	427	GCAGAACCAACGAGGTGGCCGAATCTTCTTCAAGATATCAAGAACACAGACTGTGATGA	486				
QY	386	CTGGAGAGCGGGCTGAATGCAATGGAGTGTGCATTACATTGGAAAAAATGTGAATCA	445				

Db 487 GTGGAGAGCGGCTGAATGCAATGAGTGTGCTATACATTGGGAAAAAATGTGAATCA 546  
Qy 446 GTCACTACTGGAATCC 462  
Db 547 GTCACTACTGGAATGC 563

## RESULT 2

US-09-643-597-307  
; Sequence 307, Application US/09643597  
; Patent No. 6426072

## GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: McNeill, Patricia D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: AND DIAGNOSIS OF LUNG CANCER

; CURRENT APPLICATION NUMBER: US/09/643,597

; CURRENT FILING DATE: 2000-08-21

; NUMBER OF SEQ ID NOS: 369

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 307

; LENGTH: 491

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-643-597-307

Query Match 39.3%; Score 350; DB 3; Length 491;  
Best Local Similarity 100.0%; Pred. No. 2.7e-100;  
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 86 CCGCTCTCTTCTAGTCGCGGCATGACGACCGCTCCACCTCGCAGGTGCGCCAGAACTA 145  
Db 142 CCGCTCTCTTCTAGTCGCGGCATGACGACCGCTCCACCTCGCAGGTGCGCCAGAACTA 201  
Qy 146 CCACGAGACTCAGAGCGCGCATCAACCGCAGATCAACCTGGAGCTCTACGCTCTCCTA 205  
Db 202 CCACGAGACTCAGAGCGCGCATCAACCGCAGATCAACCTGGAGCTCTACGCTCTCCTA 261  
Qy 206 CGTTTACCTGCTCCATGCTTACTACTTTTGAACCGCATGATGGCTTTGAAGAACTTTGC 265  
Db 262 CGTTTACCTGCTCCATGCTTACTACTTTTGAACCGCATGATGGCTTTGAAGAACTTTGC 321  
Qy 266 CAATATCTTCTTCCATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 325  
Db 322 CAATATCTTCTTCCATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 381  
Qy 326 GCAGAACCAACGAGGTGCGGATCTTCTTCCAGATATCAAGAAACAGACTGTGATGA 385  
Db 382 GCAGAACCAACGAGGTGCGGATCTTCTTCCAGATATCAAGAAACAGACTGTGATGA 441  
Qy 386 CTGGAGAGCGGCTGAATGCAATGAGTGTGCTATACATTGGAAAAA 435  
Db 442 CTGGAGAGCGGCTGAATGCAATGAGTGTGCTATACATTGGAAAAA 491

## RESULT 3

US-09-480-884A-307  
; Sequence 307, Application US/09480884A  
; Patent No. 6482597

## GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liqun

Query Match 39.3%; Score 350; DB 4; Length 491;  
Best Local Similarity 100.0%; Pred. No. 2.7e-100;  
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; APPLICANT: Hosken, Nancy A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY  
; FILE REFERENCE: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C6  
; CURRENT APPLICATION NUMBER: US/09/480,884A  
; CURRENT FILING DATE: 2001-08-27  
; NUMBER OF SEQ ID NOS: 330  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 307  
; LENGTH: 491  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-480-884A-307

Query Match 39.3%; Score 350; DB 4; Length 491;

Best Local Similarity 100.0%; Pred. No. 2.7e-100;  
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 86 CCGCTCTCTTCTAGTCGCGGCATGACGACCGCTCCACCTCGCAGGTGCGCCAGAACTA 145  
Db 142 CCGCTCTCTTCTAGTCGCGGCATGACGACCGCTCCACCTCGCAGGTGCGCCAGAACTA 201  
Qy 146 CCACGAGACTCAGAGCGCGCATCAACCGCAGATCAACCTGGAGCTCTACGCTCTCCTA 205  
Db 202 CCACGAGACTCAGAGCGCGCATCAACCGCAGATCAACCTGGAGCTCTACGCTCTCCTA 261  
Qy 206 CGTTTACCTGCTCCATGCTTACTACTTTTGAACCGCATGATGGCTTTGAAGAACTTTGC 265  
Db 262 CGTTTACCTGCTCCATGCTTACTACTTTTGAACCGCATGATGGCTTTGAAGAACTTTGC 321  
Qy 266 CAATATCTTCTTCCATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 325  
Db 322 CAATATCTTCTTCCATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 381  
Qy 326 GCAGAACCAACGAGGTGCGGATCTTCTTCCAGATATCAAGAAACAGACTGTGATGA 385  
Db 382 GCAGAACCAACGAGGTGCGGATCTTCTTCCAGATATCAAGAAACAGACTGTGATGA 441  
Qy 386 CTGGAGAGCGGCTGAATGCAATGAGTGTGCTATACATTGGAAAAA 435  
Db 442 CTGGAGAGCGGCTGAATGCAATGAGTGTGCTATACATTGGAAAAA 491

## RESULT 4

US-09-542-615A-307  
; Sequence 307, Application US/09542615A  
; Patent No. 6518256

## GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy R.

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY

; FILE REFERENCE: AND DIAGNOSIS OF LUNG CANCER

; CURRENT APPLICATION NUMBER: US/09/542,615A

; CURRENT FILING DATE: 2000-04-14

; NUMBER OF SEQ ID NOS: 350

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 307

; LENGTH: 491

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-542-615A-307

QY 86 CGGCTCTCTTAGTGGCGGCATGACGACCGCGTCCACCTCGCAGGTGGCCGAACTA 145  
|  
Db 142 CGGCTCTCTTAGTGGCGGCATGACGACCGCGTCCACCTCGCAGGTGGCCGAACTA 201  
|  
QY 146 CCACGAGACTCAGAGCGCGCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCCTA 205  
|  
Db 202 CCACGAGACTCAGAGCGCGCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCCTA 261  
|  
QY 206 CGTTTACCTGTCATGTCTTACTACTTTGACCGCGATGATGGCTTTGAAGAACTTTGC 265  
|  
Db 262 CGTTTACCTGTCATGTCTTACTACTTTGACCGCGATGATGGCTTTGAAGAACTTTGC 321  
|  
QY 266 CAAATACCTTTCTTACCACCTCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 325  
|  
Db 322 CAAATACCTTTCTTACCACCTCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 381  
|  
QY 326 GCAGAACCAACGAGTGGCGCAATCTTCTTCAGGATATCAAGAACACAGACTGTGATGA 385  
|  
Db 382 GCAGAACCAACGAGTGGCGCAATCTTCTTCAGGATATCAAGAACACAGACTGTGATGA 441  
|  
QY 386 CTGGGAGAGCGGCTGAATGCAATGGAGTGTGCATTACATTTGGAAAAA 435  
|  
Db 442 CTGGGAGAGCGGCTGAATGCAATGGAGTGTGCATTACATTTGGAAAAA 491  
|

## RESULT 5

US-09-606-421B-307  
; Sequence 307, Application US/09606421B  
; Patent No. 6531315

GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy

; APPLICANT: Fanger, Gary R.

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.455C9

; CURRENT APPLICATION NUMBER: US/09/606,421B

; CURRENT FILING DATE: 2000-06-28

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 307

; LENGTH: 491

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-606-421B-307

Query Match 39.3%; Score 350; DB 4; Length 491;  
Best Local Similarity 100.0%; Pred. No. 2.7e-100;  
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 CGGCTCTCTTAGTGGCGGCATGACGACCGCGTCCACCTCGCAGGTGGCCGAACTA 145  
|  
Db 142 CGGCTCTCTTAGTGGCGGCATGACGACCGCGTCCACCTCGCAGGTGGCCGAACTA 201  
|  
QY 146 CCACGAGACTCAGAGCGCGCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCCTA 205  
|  
Db 202 CCACGAGACTCAGAGCGCGCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCCTA 261  
|  
QY 206 CGTTTACCTGTCATGTCTTACTACTTTGACCGCGATGATGGCTTTGAAGAACTTTGC 265  
|  
Db 262 CGTTTACCTGTCATGTCTTACTACTTTGACCGCGATGATGGCTTTGAAGAACTTTGC 321  
|  
QY 266 CAAATACCTTTCTTACCACCTCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 325  
|  
Db 322 CAAATACCTTTCTTACCACCTCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 381  
|  
QY 326 GCAGAACCAACGAGTGGCGCAATCTTCTTCAGGATATCAAGAACACAGACTGTGATGA 385  
|

Db 382 GCAGAACCAACGAGTGGCGCAATCTTCTTCAGGATATCAAGAACACAGACTGTGATGA 441  
|  
QY 386 CTGGGAGAGCGGCTGAATGCAATGGAGTGTGCATTACATTTGGAAAAA 435  
|  
Db 442 CTGGGAGAGCGGCTGAATGCAATGGAGTGTGCATTACATTTGGAAAAA 491  
|

## RESULT 6

US-09-630-940B-307  
; Sequence 307, Application US/09630940B  
; Patent No. 6737514

GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy

; APPLICANT: Fanger, Gary R.

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Henderson, Robert A.

; APPLICANT: McNeill, Patricia D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.455C10

; CURRENT APPLICATION NUMBER: US/09/630,940B

; CURRENT FILING DATE: 2000-08-02

; NUMBER OF SEQ ID NOS: 367

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 307

; LENGTH: 491

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-630-940B-307

Query Match 39.3%; Score 350; DB 4; Length 491;  
Best Local Similarity 100.0%; Pred. No. 2.7e-100;  
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 CCGCTCTCTTAGTGGCGGCATGACGACCGCGTCCACCTCGCAGGTGGCCGAACTA 145  
|  
Db 142 CCGCTCTCTTAGTGGCGGCATGACGACCGCGTCCACCTCGCAGGTGGCCGAACTA 201  
|  
QY 146 CCACGAGACTCAGAGCGCGCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCCTA 205  
|  
Db 202 CCACGAGACTCAGAGCGCGCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCCTA 261  
|  
QY 206 CGTTTACCTGTCATGTCTTACTACTTTGACCGCGATGATGGCTTTGAAGAACTTTGC 265  
|  
Db 262 CGTTTACCTGTCATGTCTTACTACTTTGACCGCGATGATGGCTTTGAAGAACTTTGC 321  
|  
QY 266 CAAATACCTTTCTTACCACCTCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 325  
|  
Db 322 CAAATACCTTTCTTACCACCTCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 381  
|  
QY 326 GCAGAACCAACGAGTGGCGCAATCTTCTTCAGGATATCAAGAACACAGACTGTGATGA 385  
|  
Db 382 GCAGAACCAACGAGTGGCGCAATCTTCTTCAGGATATCAAGAACACAGACTGTGATGA 441  
|  
QY 386 CTGGGAGAGCGGCTGAATGCAATGGAGTGTGCATTACATTTGGAAAAA 435  
|  
Db 442 CTGGGAGAGCGGCTGAATGCAATGGAGTGTGCATTACATTTGGAAAAA 491  
|

## RESULT 7

US-09-919-172-94  
; Sequence 94, Application US/09919172  
; Patent No. 6673545

GENERAL INFORMATION:

; APPLICANT: Farris, Mary

; APPLICANT: Turner, Christopher M.

;; TITLE OF INVENTION: PROSTATE CANCER MARKERS  
;; FILE REFERENCE: PA-0036 US  
;; CURRENT APPLICATION NUMBER: US/09/919,172  
;; CURRENT FILING DATE: 2001-07-30  
;; PRIOR APPLICATION NUMBER: 60/222,469  
;; PRIOR FILING DATE: 2000-07-28  
;; NUMBER OF SEQ ID NOS: 102  
;; SOFTWARE: PERL Program  
;; SEQ ID NO 94  
;; LENGTH: 924  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; OTHER INFORMATION: Incyte ID No. 6673545 1382920.38  
US-09-919-172-94

Query Match 39.1%; Score 348.6; DB 4; Length 924;  
Best Local Similarity 98.4%; Pred. No. 1.1e-99;  
Matches 373; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 86 CGGCTCTCCTTAGTCGCGCCCATGACGACCGCGTCCACCT-CGCAGGTG-CGCCAGAAC 143  
DB 184 COTCCTTTCTTCTTAGTCGCGCCCATGACGACCGCGTCCACCTCGCGCAGGTGCGCCAGAAC 243  
QY 144 TACCACGAGGACTCAGAGGCGCCCATCAACCGCCAGATCAACCTGGAGCTCTACGCCCTCC 203  
DB 244 TACCACGAGGACTCAGAGGCGCCCATCAACCGCCAGATCAACCTGGAGCTCTACGCCCTCC 303  
QY 204 TAGCTTTACCTGTCATGCTTACTTACCTTTGACCGCGATGATGGCTTTGAAGAATTT 263  
DB 304 TAGCTTTACCTGTCATGCTTACTTACTTGTGACCGCGATGATGGCTTTGAAGAATTT 363  
QY 264 GCCAATACTTTCTTACCACCTCTCATGAGGAGGGAACATCTTGAGAACTGATGAAG 323  
DB 364 GCCAATACTTTCTTACCACCTCTCATGAGGAGGGAACATCTTGAGAACTGATGAAG 423  
QY 324 CTGCAGAACCAACGAGGTGGCGGAATCTTCTTCAGGATATCAAGAAACCGAGCTGTGAT 383  
DB 424 CTGCAGAACCAACGAGGTGGCGGAATCTTCTTCAGGATATCAAGAAACCGAGCTGTGAT 483  
QY 384 GACTGGGAGGCGGCTGAATGCAATGAGTGTGCATTACATTTGGAAAAAATGTGAAT 443  
DB 484 GACTGGGAGGCGGCTGAATGCAATGAGTGTGCATTACATTTGGAAAAAATGTGAAT 543  
QY 444 CAGTCACTACTGGAATTC 462  
DB 544 CAGTCACTACTGGAATTC 562

RESULT 8  
US-09-976-594-1076  
; Sequence 1076, Application US/09976594  
; Patent No. 6673549  
; GENERAL INFORMATION:  
; APPLICANT: Furness, Michael  
; APPLICANT: Buchbinder, Jenny  
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS  
; FILE REFERENCE: PA-0041 US  
; CURRENT APPLICATION NUMBER: US/09/976,594  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: 60/240,409  
; PRIOR FILING DATE: 2000-10-12  
; NUMBER OF SEQ ID NOS: 1143  
; SOFTWARE: PERL Program  
; SEQ ID NO 1076  
; LENGTH: 924  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. 6673549 1382920.38  
US-09-976-594-1076

Query Match 39.1%; Score 348.6; DB 4; Length 924;  
Best Local Similarity 98.4%; Pred. No. 1.1e-99;  
Matches 373; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 86 CGGCTCTCCTTAGTCGCGCCCATGAGGACCGGTCCACCT-CGCAGGTG-CGCCAGAAC 143  
DB 184 COTCCTTTCTTCTTAGTCGCGCCCATGAGGACCGGTCCACCTCGCGCAGGTGCGCCAGAAC 243  
QY 144 TACCACGAGGACTCAGAGGCGCCCATCAACCGCCAGATCAACCTGGAGCTCTACGCCCTCC 203  
DB 244 TACCACGAGGACTCAGAGGCGCCCATCAACCGCCAGATCAACCTGGAGCTCTACGCCCTCC 303  
QY 204 TAGCTTTACCTGTCATGCTTACTTACTTGTGACCGCGATGATGGCTTTGAAGAATTT 263  
DB 304 TAGCTTTACCTGTCATGCTTACTTACTTGTGACCGCGATGATGGCTTTGAAGAATTT 363  
QY 264 GCCAATACTTTCTTACCACCTCTCATGAGGAGGGAACATCTTGAGAACTGATGAAG 323  
DB 364 GCCAATACTTTCTTACCACCTCTCATGAGGAGGGAACATCTTGAGAACTGATGAAG 423  
QY 324 CTGCAGAACCAACGAGGTGGCGGAATCTTCTTCAGGATATCAAGAAACCGAGCTGTGAT 383  
DB 424 CTGCAGAACCAACGAGGTGGCGGAATCTTCTTCAGGATATCAAGAAACCGAGCTGTGAT 483  
QY 384 GACTGGGAGGCGGCTGAATGCAATGAGTGTGCATTACATTTGGAAAAAATGTGAAT 443  
DB 484 GACTGGGAGGCGGCTGAATGCAATGAGTGTGCATTACATTTGGAAAAAATGTGAAT 543  
QY 444 CAGTCACTACTGGAATTC 462  
DB 544 CAGTCACTACTGGAATTC 562

RESULT 9  
US-09-949-016-14890/C  
; Sequence 14890, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14890  
; LENGTH: 93364  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(93364)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-14890

Query Match 38.4%; Score 341.8; DB 4; Length 93364;  
Best Local Similarity 94.2%; Pred. No. 2.7e-96;  
Matches 355; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 86 CGGCTCTCCTTAGTCGCGCCCATGAGGACCGGTCCACCTCGCGCAGGTGCGCCAGAATA 145  
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QY 146 CCACCGAGGACTCAGAGGCGCCCATCAACCGCCAGATCAACCTGGAGCTCTACGCCCTCTTA 205  
|||||

Db 40844 CCACCAGGACTCAGAGCGGCCCATCAACGGCCAGATCAACCTGGAGCTCTACGCCCTCCTA 40785  
Qy 206 CGTTTACCTGTCATGCTTACTACTTTGACCGCCGATGATGGCTTTGAAGAACTTTGC 265  
Db 40784 CGTTTACCTGTCGATGCTTACAACTTTGACCGCGATGATGGCTTTGAGGAACCTTTGC 40725  
Qy 266 CAAATACCTTTCTTACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 325  
Db 40724 CACATACTTTCTTACCAATCTCATGAGGAGGGAACATGCGGAGAACTGATGAAGCT 40665  
Qy 326 GCAGAACCAACGAGGTGGCGGAATCTTCTTCAGGATATCAAGAAACAGACTGTGATGA 385  
Db 40664 GCAGAACATATGCTGGTGGCCAAATCTTCTTCAGGATATCAAGAAACAGCTGTGATGA 40605  
Qy 386 CTGGAGAGCGGCTGGAATGCAATGAGTGTGCATTTGAAAAAATGGAATCA 445  
Db 40604 CTGGAGAGTGGGCTGGAATGCAATGAGTGTGCATTTGAAAAAATGGAATCA 40545  
Qy 446 GTCACTACTGGAATTC 462  
Db 40544 GTCACTATTTGGAATGTC 40528

## RESULT 10

US-09-799-451-404  
; Sequence 404, Application US/09799451  
; Patent No. 6783969

## GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom  
; APPLICANT: Zhou, Ping  
; APPLICANT: Goodrich, Ryle  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Zhang, Jie  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Ma, Yunqing  
; APPLICANT: Yamazaki, Victoria  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Ghosh, Reena  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and  
; FILE REFERENCE: 803  
; CURRENT APPLICATION NUMBER: US/09/799,451  
; CURRENT FILING DATE: 2001-03-05  
; NUMBER OF SEQ ID NOS: 948  
; SOFTWARE: pt FL\_genes Version 2.0  
; SEQ ID NO 404  
; LENGTH: 933  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (155)..(694)

US-09-799-451-404

Query Match 34.7%; Score 309.6; DB 4; Length 933;

Best Local Similarity 90.7%; Pred. No. 2.4e-87;

Matches 330; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 99 GTCGCGGCATGACGACCGCTCCACCTCGCAGGTGGCGCAGAACTACCAAGACTCA 158  
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Qy 159 GAGGCGGCATCAACCGCCAGATCAACCTGGAGCTCTACGCCCTCTACGTTTACCTGTC 218  
Db 206 GAGGCTGCCATCAACCGCCAGATCAACCTGGAGTGTATGCTCTCTATCTGTCT 265

Qy 219 ATGCTTACTACTTTGACCGGATGATGCTGCTTTGAAGAACTTTGCCAAATACTTTCTT 278  
Db 266 ATGCTTGTATTATTTGACCGGATGATGCTGCTTTGAAGAACTTTGCCAAATACTTTCTC 325  
Qy 279 CACCAATCTCATGAGGAGGGAACATGCTGAGAAACTGATGAAGCTGCAGAAACCAACGA 338  
Db 326 CACCAATCTCATGAGGAGGGAACATGCCGAGAACTGATGAAGCTGCAGAAACCAACGA 385  
Qy 339 GGTGGCGGAATCTTCTTCAGGATATCAAGAAACAGACTGTGATGACTGGGAGAGCGGG 398  
Db 386 GGTGGCGGAATCTTCTTCAGGATATCAAGAAACAGACTGTGATGACTGGGAGAGCGGG 445  
Qy 399 CTGAATGCAATGGAGTGTGCATTTGAAAAAATGGAATCAGTCACTACTGNA 458  
Db 446 CTGAATGCAATGGAGTGTGCATTTGAAAAAAGAGTGTGAATCAGTCACTACTGNA 505  
Qy 459 TTCC 462  
Db 506 CTGC 509

## RESULT 11

US-09-949-016-12136  
; Sequence 12136, Application US/09949016  
; Patent No. 6812339

## GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12136  
; LENGTH: 32065  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(32065)  
; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-12136

Query Match 32.9%; Score 293; DB 4; Length 32065;

Best Local Similarity 87.3%; Pred. No. 3.9e-81;

Matches 357; Conservative 0; Mismatches 20; Indels 32; Gaps 2;

Qy 86 CCGCTCTCTTAGTGGCGGCATGACGACCGGCTCCACCTCGCAGGTGGCGCAGACTA 145  
Db 17986 CCGCTCTCTTAGTGGCGGCATGACGACCGGCTCTACCTCGCAGGTGGCGCAGACTA 18045  
Qy 146 CCACGAGACTCAGAGCGCGCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCTCTA 205  
Db 18046 CCACGAGACTCAGAGCGCGCATCAACCGCCAGATCAACCTGGAGCTCTACGCTCTCTC 18105  
Qy 206 CGTTTACCTGCTTACTTACTTACTTTGACCGGATGATGGCTTTGAAGAACTTTGC 265  
Db 18106 CATTTACCTGCTGGCTTACTTACTTTGACCGGATGATGGCTTTGAAGAACTTTGC 18165  
Qy 266 CAAATATCTTCTTACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 325  
Db 18166 CAAATATCTTCTTACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 18225  
Qy 326 GCAGAACCAAGAGTGGCGCAATCTTCTTCAGGATATCAAGAAACAGACTGTGATG- 384

Db 18226 GTAGAACCAACGAGGTGGCCGAATCTTCTTCAGGATATCAAGAAACAGACTGTGGGG 18285  
Qy 385 -----ACTGGGAGCGGCTGAATGCAATGG-----AG 413  
Db 18286 GAGATGCGATGGGAGCGGCTGAATGCGATGATACATTTGGAAAAAATTTGTGCAT 18345  
Qy 414 TGTGCATTACATTTGGAAAAAATTTGTAATCAGTCACCTACTGGAATTC 462  
Db 18346 TTTGCATTACATTTGGAAAAAATTTGTAATCAGTCACCTACTGGAATTC 18394  
RESULT 12  
US-09-949-016-13268  
; Sequence 13268, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13268  
; LENGTH: 32066  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(32066)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-13268  
Query Match 32.9%; Score 293; DB 4; Length 32066;  
Best Local Similarity 87.3%; Pred. No. 3.9e-81;  
Matches 357; Conservative 0; Mismatches 20; Indels 32; Gaps 2;  
Qy 86 CGCCTCTCTTCTAGTCGGCGGCATGACGACCGCGTCCACCTCGCAGGTGCGCCGAACTA 145  
Db 17986 CGCCTCTCTTCTAGTCGGCGGCATGACGACCGCGTCTACCTCGCAGGTGCGCCGAACTA 18045  
Qy 146 CCACGAGACTCAGAGCGCGGCATCAACCGCCAGATCAACCTGGAGCTCTAGCCTCCTA 205  
Db 18046 CCACCAAGACTCAGAGCGCGGCATCAACCGCCAGATCAACCTGGAGCTCTAGCCTCCTC 18105  
Qy 206 GGTTTACCTGTCATGTCTTACTACTTTGACCGCGATGATGGCTTTGAAGAACTTGC 265  
Db 18106 CATTTACCTGTCGGTGTCTTACTTTGACGCGCATGATGGCTTTGAAGAACTTGC 18165  
Qy 266 CAAATACCTTTCTTCCAACTCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 325  
Db 18166 CAAATACCTTTCTTCCAACTCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 18225  
Qy 326 CGAGAACCAACGAGTGGCGGAACTCTTCTTCAGGATATCAAGAACAGACTGTGATG- 384  
Db 18226 GTAGAACCAACGAGTGGCGGAACTCTTCTTCAGGATATCAAGAACAGACTGTGCGGG 18285  
Qy 385 -----ACTGGGAGCGGCTGAATGCAATGG-----AG 413  
Db 18286 GAGATGCGATGGGAGCGGCTGAATGCGATGATACATTTGGAAAAAATTTGTGCAT 18345  
Qy 414 TGTGCATTACATTTGGAAAAAATTTGTAATCAGTCACCTACTGGAATTC 462  
Db 18346 TTTGCATTACATTTGGAAAAAATTTGTAATCAGTCACCTACTGGAATTC 18394

## RESULT 13

US-09-313-294A-6635  
; Sequence 6635, Application US/09313294A  
; Patent No. 6476212  
; GENERAL INFORMATION:  
; APPLICANT: Lalgudi, Raghunath V.  
; APPLICANT: Ito, Laura Y.  
; APPLICANT: Sherman, Bradley K.  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR  
; FILE REFERENCE: PL-0017 US  
; CURRENT APPLICATION NUMBER: US/09/313,294A  
; CURRENT FILING DATE: 1999-05-14  
; NUMBER OF SEQ ID NOS: 7600  
; SOFTWARE: PERL Program  
; SEQ ID NO 6635  
; LENGTH: 292  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No. 6476212 700352138H1  
US-09-313-294A-6635

Query Match 26.6%; Score 237.2; DB 4; Length 292;  
Best Local Similarity 98.8%; Pred. No. 9.7e-65;  
Matches 239; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 221 GTCTTACTACTTTGACCGCGATGATGTGGCTTTGAAGAACTTTGCCAAATACCTTTCTTCA 280  
Db 1 GTCTTACTACTTTGACCGCGATGATGTGGCTTTGAAGAACTCTGCCAAATACCTTTCTTCA 60  
Qy 281 CCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCTGAGAACCAACGAGG 340  
Db 61 CCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCTGAGAACCAACGAGG 120  
Qy 341 TGCCGGAATCTCTTTCAGGATATCAAGAACCAAGACTGTGATCAGTGGGAGCGGGCT 400  
Db 121 TGCCGGAATCTCTTTCAGGATATCAAGAACCAAGACTGTGATCAGTGGGAGCGGGCT 180  
Qy 401 GAATGCAATGGAGTGTGCATTACATTTGGAAAAAATTTGAATCAGTCACCTACTGGAATT 460  
Db 181 GAATGCAATGGAGTGTGCATTACATTTGGAAAAAATTTGAATCAGTCACCTACTGGAATT 240  
Qy 461 CC 462  
Db 241 GC 242

## RESULT 14

US-09-949-016-115137/c  
; Sequence 115137, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 115137  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-115137





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(without alignments)  
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Sequence: 1 ttgacaccagaccactggt.....acgacaacataaaaaaa 891

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Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: gb\_on.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pi.\*  
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10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sv.\*  
13: gb\_un.\*  
14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	891	100.0	891	6	AX023297 Sequence
2	864.8	97.1	891	6	AX023293 Sequence
3	845	94.8	845	9	AY033611 Homo sapi
4	373.8	42.0	567	6	AX381667 Sequence
5	373.8	42.0	708	9	AF088851 Homo sapi
6	373.8	42.0	737	9	M12937 Human ferri
7	373.8	42.0	788	9	BC015156 Homo sapi
8	373.8	42.0	790	6	BD094093 Shear str
9	373.8	42.0	790	6	HUMFERH
10	373.8	42.0	801	6	C0834024 Sequence
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12	373.8	42.0	804	6	CQ729634 Sequence
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14	373.8	42.0	884	9	BC016857 Homo sapi
15	373.8	42.0	900	9	BC001399 Homo sapi
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27	373.8	41.9	791	6	AX381974	Sequence
28	373	41.9	1119	9	HUMFERRH	
29	373	41.9	1198	6	AX409527	Sequence
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33	372.2	41.8	938	9	AB062402	Homo sapi
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35	371	41.6	593	6	AX381566	Sequence
36	370.6	41.6	839	9	BC066341	Homo sapi
37	370.6	41.6	3621	9	AK127090	Homo sapi
38	367	41.2	545	6	AX381649	Sequence
39	367	41.2	550	6	AX381676	Sequence
c 40	361.8	40.6	654	6	AX255859	Sequence
41	361	40.5	161786	9	AC104820	Homo sapi
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c 44	357.8	40.2	168114	9	AL354828	Human DNA
45	353	39.6	803	6	CQ722476	Sequence

ALIGNMENTS

RESULT 1  
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LOCUS AX023297 891 bp DNA linear PAT 15-SEP-2000  
DEFINITION Sequence 5 from Patent WO0015788.  
ACCESSION AX023297  
VERSION AX023297.1 GI:10183710  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 Moroz,C.  
AUTHORS  
TITLE Dna sequence encoding oncofetal ferritin protein  
JOURNAL Patent: WO 0015788-A 5 23-MAR-2000;  
MOROS CHAYA (IL) ; GARDINO INVESTMENT N V (NL)  
FEATURES  
Location/Qualifiers  
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Db	1	TTGACACAGACCACTGGTAATGTAGTACGACCGCGCTCAGCTGGAATTCACAAAATG	60							
Qy	61	TAATGCACATCCCATTTGCATTCAGCCCGCTCTCTTCTAGTCCGCCCATGACACCGCT	120							
Db	61	TAATGCACATCCCATTTGCATTCAGCCCGCTCTCTTCTAGTCCGCCCATGACACCGCT	120							
Qy	121	CCACTCGCAGGTGCGCCAGAACTACACAGGACTCAGAGCCGCCCATCAACCGCGAGA	180							
Db	121	CCACTCGCAGGTGCGCCAGAACTACACAGGACTCAGAGCCGCCCATCAACCGCGAGA	180							
Qy	181	TCAACCTGGAGCTCTACGCTCCTACCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	240							
Db	181	TCAACCTGGAGCTCTACGCTCCTACCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	240							

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Db 301 AACATGCTGAGAACTGATGAGCTGACAGAACCAACAGAGGTGGCGAATCTTCTTTCAGG 360
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Db 481 GTCTAGTGTGGCATCACTATCTACTACAGACCGCAACCTCAACACACCTTCTTC 540
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Db 841 GTTTTCACACTCTAGTAGAGCTTACCTGACGACACACATATAAAAAA 891
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RESULT 2
AX023293 AX023293 891 bp DNA linear PAT 15-SEP-2000
LOCUS Sequence 1 from Patent WO0015788.
DEFINITION AX023293
ACCESSION AX023293
VERSION AX023293.1 GI:10183706
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1.
AUTHORS Moroz,C.
TITLE Dna sequence encoding oncofetal ferritin protein
JOURNAL Patent: WO 0015788-A 1 23-MAR-2000;
MOROS CHAYA (IL); GARDINO INVESTMENT N V (NL)
FEATURES
Location/Qualifiers
source
1. 891
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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## ORIGIN

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Query Match 97.1%; Score 864.8; DB 6; Length 891;
Best Local Similarity 99.6%; Pred. No. 1.2e-217;
Matches 888; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
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Db 61 TAATGACACACTCCATTGGCAATTCAGCCCGCTCTCTTAGTCGGCGGCATGACGACCGCG 119
QY 120 TCCACCTCGCAGGTGCGCAGAACTACCAACAGGACTCAGAGGCGCGCATCAACCGCCAG 179
Db 120 TCCACCTCGCAGGTGCGCAGAACTACCAACAGGACTCAGAGGCGCGCATCAACCGCCAG 179
QY 180 ATCAACCTGGAGCTCTAGCGCTCTAGCTTTACCTGTCATCTTACTACTTTGACCGC 239
Db 180 ATCAACCTGGAGCTCTAGCGCTCTAGCTTTACCTGTCATCTTACTACTTTGACCGC 239
QY 240 GATCATGTGGCTTTGAAGAACTTTGCCAAATCTTTTTCACCAATCTCATGAGGAGG 299
Db 240 GATCATGTGGCTTTGAAGAACTTTGCCAAATCTTTTTCACCAATCTCATGAGGAGG 299
QY 300 GAAATGCTGAGAACTGATGAGCTGCAGAACCAACAGGTGGCGCGAATCTTCTTTCAG 359
Db 300 GAAATGCTGAGAACTGATGAGCTGCAGAACCAACAGGTGGCGCGAATCTTCTTTCAG 359
QY 360 GATATCAAGAAACAGACTGTGATGACTGGGAGAGCGGCTGAATGCAATGGAGTGTCA 419
Db 360 GATATCAAGAAACAGACTGTGATGACTGGGAGAGCGGCTGAATGCAATGGAGTGTCA 419
QY 420 TTACATTTGGAAGAAATGTAATCAGTCAGTCTGGAATTCCTCTCTCTCTCTCTCTCC 479
Db 420 TTACATTTGGAAGAAATGTAATCAGTCAGTCTGGAATTCCTCTCTCTCTCTCTCTCC 479
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DEFINITION AX033611
ACCESSION AX033611
VERSION AX033611.1 GI:20127144
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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**REFERENCE**  
**AUTHORS**  
**TITLE**  
**JOURNAL**  
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**TITLE**  
**JOURNAL**  
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Qy	707	AC	TACTATGC	ACCTAATT	TGGAAGCCAC	CCCTAGCAATATCAACCA	TTAACCTTCCCT	766
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LOCUS					Sequence 605	from Patent	WO0212280.	
DEFINITION					AX381667			
ACCESSION					AX381667.1	GI:19576489		
VERSION								
KEYWORDS								
SOURCE					Homo sapiens (human)			
ORGANISM					Homo sapiens			
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AUTHORS					Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
TITLE					1. Pyle, R.A., Xu, J. and Secrist, H.			
JOURNAL					Compositions and methods for the therapy and diagnosis of colon cancer			
FEATURES					Patent: WO 0212280-A 605 14-FEB-2002;			
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LOCUS Homo sapiens ferritin heavy chain subunit mRNA, complete cds.
DEFINITION Homo sapiens ferritin heavy chain subunit mRNA, complete cds.
ACCESSION AF088851
VERSION AF088851.1 GI:9621743
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 708)
AUTHORS Franco,A.V., Gray,C.P., Myers,K. and Hersey,P.
TITLE Detection of ferritin heavy chain by serex: A multifunctional
molecule in malignant tumour cells
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 708)
AUTHORS Franco,A.V., Gray,C.P., Myers,K. and Hersey,P.
TITLE Direct Submission
JOURNAL Submitted (30-AUG-1998) Oncology and Immunology, Royal Newcastle
Hospital, Cnr King and Watt Streets, Newcastle, N.S.W 2300,
Australia

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Best Local Similarity 99.5%; Pred. No. 9.8e-88;
Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 86 CCGCTCTCTTGTAGTCGCGCATGACGACCGGTCCACCTCGAGGTGCGCCAGAACTA 145
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RESULT 6
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LOCUS Human ferritin heavy subunit mRNA, complete cds.
DEFINITION Human ferritin heavy subunit mRNA, complete cds.
ACCESSION M12937
VERSION M12937.1 GI:182506
KEYWORDS ferritin.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 737)
AUTHORS Chou,C.C., Gatti,R.A., Fuller,M.L., Concannon,P., Wong,A.,
Chada,S., Davis,R.C. and Salser,W.A.
TITLE Structure and expression of ferritin genes in a human promyelocytic
cell line that differentiates in vitro
JOURNAL Mol. Cell. Biol. 6 (2), 566-573 (1986)
MEDLINE 87064341
PUBMED 3023856
COMMENT Original source text: Human promyelocytic cell line HL-60 cDNA to
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Query Match 42.0%; Score 373.8; DB 9; Length 737;
Best Local Similarity 99.5%; Pred. No. 9.8e-88;
Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 ACCESSION BC015156  
 VERSION BC015156.1 GI:15929450  
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 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
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 Strausberg,R.L., Feingold,B.A., Grouse,L.H., Derge,J.G.,  
 Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,  
 Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,  
 Hopkins,R.P., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,  
 Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,  
 Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,  
 Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,  
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 Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y.,  
 Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,  
 Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,  
 Butlerfield,Y.S., Krzywinski,M.I., Skalska,U., Smalish,D.E.,  
 Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
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 Strausberg,R.  
 Direct Submission  
 Submitted (01-OCT-2001) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
 Tissue Procurement: DCTD/DP/Gapdar  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome  
 Center, Stanford University School of Medicine, Stanford, CA 94305  
 Web site: <http://www-shgc.stanford.edu>  
 Contact: (Dickson, Mark) [mcdpaxil.stanford.edu](mailto:mcdpaxil.stanford.edu)  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
 R. M.

Clone distribution: MGC clone distribution information can be found  
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## ORIGIN

Query Match 42.0%; Score 373.8; DB 9; Length 788;  
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 QY 86 CCGCTCTCTTAGTGGCGGCATGACGACCGGTCCACCTCGCAGGTGGCCAGAACTA 145  
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 ACCESSION BD094093.1 GI:22639681  
 VERSION BD094093.1  
 KEYWORDS WO 0125427-A/54.

BD094093 790 bp DNA linear PAT 27-AUG-2002  
 Shear stress-responsive DNAs.  
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DEFINITION Sequence 60 from Patent EP1439393.  
ACCESSION CQ834024  
VERSION CQ834024.1 GI:50833629  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Asle, J.H., Boardman, L.A., Bugart, L.J., Burgess, C.C., Catino, T.J.,  
Dwivedi, P., Huntress, M., Johnson, K.A., Lewis, M.E., Maimonis, P.J.,  
Myerow, S.H., Brown-Shimer, S.L., Thiagalingam, A., Thibodeau, S.N. and  
Molino, G.A.  
TITLE Detection methods using TIMP 1 for colon cancer diagnosis  
JOURNAL Patent: EP 1439393-A 60 21-JUL-2004;  
Bayer Healthcare LLC (US); MAYO FOUNDATION FOR MEDICAL EDUCATION  
AND RESEARCH (US)

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Best Local Similarity 99.5%; Pred. No. 1e-87; Indels 0; Gaps 0;  
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Qy 386 CTGGAGAGCGGCTGAATGCAATGGAGTGCATTATTTGGAAGAAATGTAATCA 445  
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Qy 446 GTCACCTACTGGAATTC 462  
Db 430 GTCACCTACTGGAAGTGC 446

RESULT 11  
LOCUS HSAFH1  
DEFINITION Human mRNA for apoferritin H chain type.  
ACCESSION X00318  
VERSION X00318.1 GI:28434  
KEYWORDS apoferritin.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS Costanzo, F., Santoro, C., Colantuoni, V., Bensi, G., Raugei, G.,  
Romano, V. and Cortese, R.  
TITLE Cloning and sequencing of a full length cDNA coding for a human  
apoferritin H chain: evidence for a multigene family  
JOURNAL EMBO J. 3 (1), 23-27 (1984)  
MEDLINE 84158535  
PUBMED 6323167

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polyA\_site  
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Best Local Similarity 99.5%; Pred. No. 1e-87; Indels 0; Gaps 0;  
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Db 430 GTCACCTACTGGAAGTGC 446

RESULT 12  
LOCUS CQ729634  
DEFINITION Sequence 15568 from Patent WO2068579.  
ACCESSION CQ729634  
VERSION CQ729634.1 GI:42301253  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

804 bp DNA linear PAT 03-FEB-2004

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

## AUTHORS

Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.  
Kits, such as nucleic acid arrays, comprising a majority of  
humanexons or transcripts, for detecting expression and other uses  
thereof

## JOURNAL

Patent: WO 02068579-A 15568 06-SEP-2002;

## PE CORPORATION

(NY) (US)

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1. .804

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

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Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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QY 326 GCAGAACCAACGAGGTGCGCGAATCTCTTACGATATCAAGAACAGACTGTGATGA 385  
DB 310 GCAGAACCAACGAGGTGCGCGAATCTCTTACGATATCAAGAACAGACTGTGATGA 369  
QY 386 CTGGAGAGCGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATCA 445  
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QY 446 GTCACTACTGGAATCC 462  
DB 430 GTCACTACTGGAATCC 446

## RESULT 13

## BC070494

## LOCUS

BC070494 856 bp mRNA linear PRI 11-MAY-2004  
Homo sapiens ferritin, heavy polypeptide 1, mRNA (cdna clone  
IMAGE:6009374), partial cds.

## DEFINITION

## ACCESSION

## BC070494

## VERSION

## BC070494.1

## KEYWORDS

## SOURCE

## Homo sapiens

## (human)

## ORGANISM

## Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

## AUTHORS

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
Klauser, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
Hopkins, R.F., Jordan, H., Moore, I., Max, S.I., Wang, J., Hsieh, F.,  
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,  
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
Abramson, R.D., Mullaby, S.J., Bosak, S.A., McEwan, P.J.,  
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
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Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,  
Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D.,  
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalhus, D.E.,  
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
2 (bases 1 to 856)  
Strausberg, R.  
Direct Submission  
Submitted (10-MAY-2004) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgaps-x@mail.nih.gov](mailto:cgaps-x@mail.nih.gov)  
Tissue Procurement: DCTD/DTP/Gazdar  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>  
Contact: [nisc\\_mgc@hgrl.nih.gov](mailto:nisc_mgc@hgrl.nih.gov)  
Akhter, N., Ayete, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,  
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghghi, P.,  
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,  
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,  
McDowell, J., Pearson, R., Stantropop, S., Thomas, P.J., Touchman, J.W.,  
Tsurgon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,  
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAC Plate: 174 Row: e Column: 18  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 4503794.  
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## /lab\_host="DH10B"

## /note="Vector: pCMV-SPORT6"

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DB 488 GTCACCTACTGGAATTC 504

RESULT 14
LOCUS BC016857
DEFINITION Homo sapiens ferritin, heavy polypeptide 1, mRNA (cdna clone
MGC:17216 IMAGE:3848510), complete cds.
ACCESSION BC016857
VERSION BC016857.1 GI:16877183
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 884)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heideh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toehiyuki,S.,
Carninci,P., Prange,C., Raha,S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalish,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
MEDLINE 12477932
PUBMED
REFERENCE 2 (bases 1 to 884)
Strausberg,R.
AUTHORS
Direct Submission
TITLE
Submitted (05-NOV-2001) National Institutes of Health, Mammalian
```

```
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-sbqc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
Series: IPAK Plate: 20 Row: j Column: 8
This clone was selected for full length sequencing because it
passed the following selection criteria: Genomescan gene
prediction, Similarity but not identity to protein.

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Best Local Similarity 99.5%; Pred. No. 1e-87;
Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 86 CCGCTCTCTCTAGTTCGGCGCATGACACCGCGTCCACCTCGCAGGTGCGCGAAGCTA 145
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## RESULT 2

US-09-918-995-27591  
; Sequence 27591, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 27591  
; LENGTH: 583  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)-(583)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-918-995-27591

Query Match 42.0%; Score 373.8; DB 10; Length 583;  
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US-10-278-698-128  
; Sequence 128, Application US/10278698  
; Publication No. US20050037344A1  
; GENERAL INFORMATION:  
; APPLICANT: PathoArray GmbH  
; APPLICANT: Stuhlmüller, Bruno  
; APPLICANT: Haupt, Thomas  
; TITLE OF INVENTION: Nucleic Acid Array  
; FILE REFERENCE: O30027US  
; CURRENT APPLICATION NUMBER: US/10/278,698  
; CURRENT FILING DATE: 2002-10-23  
; NUMBER OF SEQ ID NOS: 1050  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 128  
; LENGTH: 790  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-278-698-128

Query Match 42.0%; Score 373.8; DB 19; Length 790;  
Best Local Similarity 99.5%; Pred. No. 2e-110;  
Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 86 CGCCTCTCTTACTGTCGCGGCATGACACCGCGTCCACCTCGCAGGTGCGCCAGAACTA 145  
Db 56 CGCCTCTCTTACTGTCGCGGCATGACACCGCGTCCACCTCGCAGGTGCGCCAGAACTA 115  
Qy 146 CCACGAGACTCAGAGGCGGCATCAACCGCCAGATCAACCTGGAGCTTACGCTCCTA 205  
Db 116 CCACGAGACTCAGAGGCGGCATCAACCGCCAGATCAACCTGGAGCTTACGCTCCTA 175  
Qy 206 CGTTTACCTGTCCATGTCTTACTACTTTGACCGCATGATGCGCTTTGAAGAACTTTGC 265  
Db 176 CGTTTACCTGTCCATGTCTTACTACTTTGACCGCATGATGCGCTTTGAAGAACTTTGC 235  
Qy 266 CAAATACCTTTCTTACCAATCTCATGAGAGGGAACATGCTGAGAACTGATGAAGCT 325  
Db 236 CAAATACCTTTCTTACCAATCTCATGAGAGGGAACATGCTGAGAACTGATGAAGCT 295  
Qy 326 GCAGAACCAACGAGGTGCGGCAATCTTCTTCAGGATATCAAGAACCCAGACTGTGATGA 385  
Db 296 GCAGAACCAACGAGGTGCGGCAATCTTCTTCAGGATATCAAGAACCCAGACTGTGATGA 355  
Qy 386 CTGGGAGAGCGGCTGAATGCAATGGAGTGTGCATTACATTTGGAAAAAATGTGAATCA 445  
Db 356 CTGGGAGAGCGGCTGAATGCAATGGAGTGTGCATTACATTTGGAAAAAATGTGAATCA 415  
Qy 446 GTCACTACTGGAATTC 462  
Db 416 GTCACTACTGGAATTC 432

## RESULT 4

US-10-278-698-644  
; Sequence 644, Application US/10278698  
; Publication No. US20050037344A1  
; GENERAL INFORMATION:  
; APPLICANT: PathoArray GmbH  
; APPLICANT: Stuhlmüller, Bruno  
; APPLICANT: Haupt, Thomas  
; TITLE OF INVENTION: Nucleic Acid Array  
; FILE REFERENCE: O30027US  
; CURRENT APPLICATION NUMBER: US/10/278,698

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; CURRENT FILING DATE: 2002-10-23
; NUMBER OF SEQ ID NOS: 1050
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 644
; LENGTH: 790
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-278-698-644

Query Match      42.0%; Score 373.8; DB 19; Length 790;
Best Local Similarity 99.5%; Pred. No. 2e-110;
Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 86 CCGCTCTCTTCTAGTCGGCGGCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGAACTA 145
DB 56 CCGCTCTCTTCTAGTCGGCGGCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGAACTA 115
QY 146 CCACCAGGACTCAGAGGCGGCATCAACCGCCAGATCAACCTGGAGCTCTACGCCCTCCTA 205
DB 116 CCACCAGGACTCAGAGGCGGCATCAACCGCCAGATCAACCTGGAGCTCTACGCCCTCCTA 175
QY 206 CGTTTACCTGTCATGTCTTACTACTTTTGAACGCGATGATGGCTTTGAAGAACTTTGC 265
DB 176 CGTTTACCTGTCATGTCTTACTACTTTTGAACGCGATGATGGCTTTGAAGAACTTTGC 235
QY 266 CAAATACCTTTCTTACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 325
DB 236 CAAATACCTTTCTTACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 295
QY 326 CGAGAACCAACGAGGTGGCGGAACTCTCTTCCAGGATATCAAGAAACCCAGACTGTGATGA 385
DB 296 CGAGAACCAACGAGGTGGCGGAACTCTCTTCCAGGATATCAAGAAACCCAGACTGTGATGA 355
QY 386 CTGGAGAGCGGGCTCAATGCAATGGAGTGTGCATTACATTTGGAAGAACTTTGAATCA 445
DB 356 CTGGAGAGCGGGCTCAATGCAATGGAGTGTGCATTACATTTGGAAGAACTTTGAATCA 415
QY 446 GTCACTACTGGAATTC 462
DB 416 GTCACTACTGGAATTC 432

RESULT 5
US-10-734-564-60
; Sequence 60, Application US/10734564
; Publication No. US20040157278A1
; GENERAL INFORMATION:
; APPLICANT: Christopher C Burgess et al
; TITLE OF INVENTION: Detection Methods Using TIMP1
; FILE REFERENCE: 1657/2012
; CURRENT APPLICATION NUMBER: US/10/734,564
; CURRENT FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 801
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-734-564-60

Query Match      42.0%; Score 373.8; DB 18; Length 801;
Best Local Similarity 99.5%; Pred. No. 2e-110;
Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 86 CCGCTCTCTTCTAGTCGGCGGCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGAACTA 145
DB 70 CCGCTCTCTTCTAGTCGGCGGCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGAACTA 129
QY 146 CCACCAGGACTCAGAGGCGGCATCAACCGCCAGATCAACCTGGAGCTCTACGCCCTCCTA 205
DB 130 CCACCAGGACTCAGAGGCGGCATCAACCGCCAGATCAACCTGGAGCTCTACGCCCTCCTA 189
QY 206 CGTTTACCTGTCATGTCTTACTACTTTTGAACGCGATGATGGCTTTGAAGAACTTTGC 265

; CURRENT FILING DATE: 2002-10-23
; NUMBER OF SEQ ID NOS: 1050
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 644
; LENGTH: 790
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-278-698-644

Query Match      42.0%; Score 373.8; DB 19; Length 790;
Best Local Similarity 99.5%; Pred. No. 2e-110;
Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 86 CCGCTCTCTTCTAGTCGGCGGCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGAACTA 145
DB 56 CCGCTCTCTTCTAGTCGGCGGCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGAACTA 115
QY 146 CCACCAGGACTCAGAGGCGGCATCAACCGCCAGATCAACCTGGAGCTCTACGCCCTCCTA 205
DB 116 CCACCAGGACTCAGAGGCGGCATCAACCGCCAGATCAACCTGGAGCTCTACGCCCTCCTA 175
QY 206 CGTTTACCTGTCATGTCTTACTACTTTTGAACGCGATGATGGCTTTGAAGAACTTTGC 265
DB 176 CGTTTACCTGTCATGTCTTACTACTTTTGAACGCGATGATGGCTTTGAAGAACTTTGC 235
QY 266 CAAATACCTTTCTTACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 325
DB 236 CAAATACCTTTCTTACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 295
QY 326 CGAGAACCAACGAGGTGGCGGAACTCTCTTCCAGGATATCAAGAAACCCAGACTGTGATGA 385
DB 296 CGAGAACCAACGAGGTGGCGGAACTCTCTTCCAGGATATCAAGAAACCCAGACTGTGATGA 355
QY 386 CTGGAGAGCGGGCTCAATGCAATGGAGTGTGCATTACATTTGGAAGAACTTTGAATCA 445
DB 356 CTGGAGAGCGGGCTCAATGCAATGGAGTGTGCATTACATTTGGAAGAACTTTGAATCA 415
QY 446 GTCACTACTGGAATTC 462
DB 416 GTCACTACTGGAATTC 432

RESULT 6
US-10-198-846-9581
; Sequence 9581, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9581
; LENGTH: 830
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 795, 801, 809
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-9581

Query Match      42.0%; Score 373.8; DB 14; Length 830;
Best Local Similarity 99.5%; Pred. No. 2e-110;
Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 86 CCGCTCTCTTCTAGTCGGCGGCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGAACTA 145
DB 56 CCGCTCTCTTCTAGTCGGCGGCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGAACTA 115
QY 146 CCACCAGGACTCAGAGGCGGCATCAACCGCCAGATCAACCTGGAGCTCTACGCCCTCCTA 205
DB 116 CCACCAGGACTCAGAGGCGGCATCAACCGCCAGATCAACCTGGAGCTCTACGCCCTCCTA 175
QY 206 CGTTTACCTGTCATGTCTTACTACTTTTGAACGCGATGATGGCTTTGAAGAACTTTGC 265
DB 176 CGTTTACCTGTCATGTCTTACTACTTTTGAACGCGATGATGGCTTTGAAGAACTTTGC 235
QY 266 CAAATACCTTTCTTACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 325
DB 236 CAAATACCTTTCTTACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 295
QY 326 CGAGAACCAACGAGGTGGCGGAACTCTCTTCCAGGATATCAAGAAACCCAGACTGTGATGA 385
DB 296 CGAGAACCAACGAGGTGGCGGAACTCTCTTCCAGGATATCAAGAAACCCAGACTGTGATGA 355
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QY 386 CTGGAGAGCGGCTGAATGCAATGAGTGTGCATTACATTGGAAAAAATGTGAATCA 445
Db 356 CTGGAGAGCGGCTGAATGCAATGAGTGTGCATTACATTGGAAAAAATGTGAATCA 415
QY 446 GTCACTACTGGAATCC 462
Db 416 GTCACTACTGGAATGC 432

RESULT 7
US-10-384-496-1
; Sequence 3, Application US/09765231A
; Patent No. US20020119452A1
; GENERAL INFORMATION:
; APPLICANT: Searle/Monsanto
; APPLICANT: Phippard, Deborah
; APPLICANT: Vasanthakamur, Geetha
; APPLICANT: Dotson, Stanton
; APPLICANT: Ma, Xiao-Jun
; TITLE OF INVENTION: Osteoarthritis tissue-derived nucleic acids, polypeptides,
; FILE REFERENCE: SO-3221 PR
; CURRENT APPLICATION NUMBER: US/09/765,231A
; CURRENT FILING DATE: 2001-01-18
; NUMBER OF SEQ ID NOS: 82
; SEQ ID NO 3
; LENGTH: 920
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-765-231A-3

Query Match 42.0%; Score 373.8; DB 9; Length 920;
Best Local Similarity 99.5%; Pred. No. 2.1e-110;
Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 86 CGGCTCTCTTCTAGTGGCGGCATGACGACCGCTCCACCTCGCAGGTGGCCGAGAACTA 145
Db 173 CGGCTCTCTTCTAGTGGCGGCATGACGACCGCTCCACCTCGCAGGTGGCCGAGAACTA 232
QY 146 CCACGAGACTCAGAGGCGGCATCAACCGCCAGATCAACCTGGAGCTCTACGCCCTCCTA 205
Db 233 CCACGAGACTCAGAGGCGGCATCAACCGCCAGATCAACCTGGAGCTCTACGCCCTCCTA 292
QY 206 CGTTTACCTGTCCATGTCTTACTACTTTGACCGCGATGATGGCTTTGAAGAACTTTGC 265
Db 293 CGTTTACCTGTCCATGTCTTACTACTTTGACCGCGATGATGGCTTTGAAGAACTTTGC 352
QY 266 CAATTAATCTTCTTCCCAATCTCATGAGGAGGGAACATGCTGAGAACTGTGAAGCT 325
Db 353 CAATTAATCTTCTTCCCAATCTCATGAGGAGGGAACATGCTGAGAACTGTGAAGCT 412
QY 326 GCAGAACCAACGAGGTGGCGGAATCTCTTCCAGGATATCAAGAAACAGACTGTGATGA 385
Db 413 GCAGAACCAACGAGGTGGCGGAATCTCTTCCAGGATATCAAGAAACAGACTGTGATGA 472
QY 386 CTGGAGAGCGGCTGAATGCAATGAGTGTGCATTACATTGGAAAAAATGTGAATCA 445
Db 473 CTGGAGAGCGGCTGAATGCAATGAGTGTGCATTACATTGGAAAAAATGTGAATCA 532
QY 446 GTCACTACTGGAATCC 462
Db 533 GTCACTACTGGAATGC 549

RESULT 8
US-10-384-496-1
; Sequence 1, Application US/10384496
; Patent No. US20030219385A1
; GENERAL INFORMATION:
; APPLICANT: AHRENS, ERIC
; TITLE OF INVENTION: CONTRAST AGENTS FOR MAGNETIC RESONANCE IMAGING AND
; FILE REFERENCE: CMV-001.01
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; CURRENT APPLICATION NUMBER: US/10/384,496
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: 60/363,163
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 955
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-384-496-1

Query Match 42.0%; Score 373.8; DB 17; Length 955;
Best Local Similarity 99.5%; Pred. No. 2.2e-110;
Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 86 CGGCTCTCTTCTAGTGGCGGCATGACGACCGCTCCACCTCGCAGGTGGCCGAGAACTA 145
Db 189 CGGCTCTCTTCTAGTGGCGGCATGACGACCGCTCCACCTCGCAGGTGGCCGAGAACTA 248
QY 146 CCACGAGACTCAGAGGCGGCATCAACCGCCAGATCAACCTGGAGCTCTACGCCCTCCTA 205
Db 249 CCACGAGACTCAGAGGCGGCATCAACCGCCAGATCAACCTGGAGCTCTACGCCCTCCTA 308
QY 206 CGTTTACCTGTCCATGTCTTACTACTTTGACCGCGATGATGGCTTTGAAGAACTTTGC 265
Db 309 CGTTTACCTGTCCATGTCTTACTACTTTGACCGCGATGATGGCTTTGAAGAACTTTGC 368
QY 266 CAATTAATCTTCTTCCCAATCTCATGAGGAGGGAACATGCTGAGAACTGTGAAGCT 325
Db 369 CAATTAATCTTCTTCCCAATCTCATGAGGAGGGAACATGCTGAGAACTGTGAAGCT 428
QY 326 GCAGAACCAACGAGGTGGCGGAATCTCTTCCAGGATATCAAGAAACAGACTGTGATGA 385
Db 429 GCAGAACCAACGAGGTGGCGGAATCTCTTCCAGGATATCAAGAAACAGACTGTGATGA 488
QY 386 CTGGAGAGCGGCTGAATGCAATGAGTGTGCATTACATTGGAAAAAATGTGAATCA 445
Db 489 CTGGAGAGCGGCTGAATGCAATGAGTGTGCATTACATTGGAAAAAATGTGAATCA 548
QY 446 GTCACTACTGGAATCC 462
Db 549 GTCACTACTGGAATGC 565

RESULT 9
US-10-071-766-9
; Sequence 9, Application US/10071766
; Publication No. US20020192678A1
; GENERAL INFORMATION:
; APPLICANT: Huel-Mei Chen
; TITLE OF INVENTION: GENES EXPRESSED IN SENESENCE
; FILE REFERENCE: PA-0043 US
; CURRENT APPLICATION NUMBER: US/10/071,766
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PERL Program
; SEQ ID NO 9
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020192678A1 1138151.17
US-10-071-766-9

Query Match 42.0%; Score 373.8; DB 13; Length 998;
Best Local Similarity 99.5%; Pred. No. 2.2e-110;
Matches 375; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 86 CGGCTCTCTTCTAGTGGCGGCATGACGACCGCTCCACCTCGCAGGTGGCCGAGAACTA 145
Db 212 CGGCTCTCTTCTAGTGGCGGCATGACGACCGCTCCACCTCGCAGGTGGCCGAGAACTA 271
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Qy	146	CCACCAGGACTCAGAGGCGCGCCATCAACCGCCAGATCAACCTGGAGCTCTACGCCCTCCTA	205
Db	272	CCACCAGGACTCAGAGGCGCGCCATCAACCGCCAGATCAACCTGGAGCTCTACGCCCTCCTA	331
Qy	206	CGTTTACCTGTGCCATGTCTTACTCTTTGACCGCGATGATGTGGCTTTTGAAGAACTTTGC	265
Db	332	CGTTTACCTGTGCCATGTCTTACTCTTTGACCGCGATGATGTGGCTTTTGAAGAACTTTGC	391
Qy	266	CAAAATCTTTCTTCAACCAATCTCATGAGGAGGGGAACAATGCTGAGAACTGATGAAGCT	325
Db	392	CAAAATCTTTCTTCAACCAATCTCATGAGGAGGGGAACAATGCTGAGAACTGATGAAGCT	451
Qy	326	GCAGAACCAACGAGGTGGCCGNACTCTTCTTCAGGATATCAGAAACCCAGACTGTGATGA	385
Db	452	GCAGAACCAACGAGGTGGCCGNACTCTTCTTCAGGATATCAGAAACCCAGACTGTGATGA	511
Qy	386	CTGGGAGAGCGGGCTGGAATGCAAATGGAGTGTGCATTACATTTGGAAAAAAATGTGAATCA	445
Db	512	CTGGGAGAGCGGGCTGGAATGCAAATGGAGTGTGCATTACATTTGGAAAAAAATGTGAATCA	571
Qy	446	GTCACACTCTGGAATTC	462
Db	572	GTCACACTCTGGAATTC	588

## RESULT 10

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RESULI 10
US-10-071-766-10
; Sequence 10, Application US/10071766
; Publication No. US20020192678A1
; GENERAL INFORMATION:
; APPLICANT: Hwei-Mei Chen
; TITLE OF INVENTION: GENES EXPRESSED IN SENESCENCE
; FILE REFERENCE: PA-0043 US
; CURRENT APPLICATION NUMBER: US/10/071,766
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PERL Program
; SEQ ID NO 10
; LENGTH: 1326
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020192678A1 1138151.2
US-10-071-766-10

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Query Match	42.0%	Score 373.8;	DB 13;	Length 1326;
Best Local Similarity	99.5%	Pred. No. 2.6e-110;		
Matches 375;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	86	CCGCGCTCTCTTAGTTCGCGCGGCATGACGACCGCGTCCACCTCGCAGGTGCGCCGCAACTA	145	
Db	136	CCGCGCTCTCTTAGTTCGCGCGCATGACGACCGCGTCCACCTCGCAGGTGCGCCGCAACTA	195	
Qy	146	CCACGAGGACTCAGAGGCGCGGCATCAACCGGCAGATCAACCTGGAGCTCTACGGCTCCTA	205	
Db	196	CCACGAGGACTCAGAGGCGCGGCATCAACCGGCAGATCAACCTGGAGCTCTACGGCTCCTA	255	
Qy	206	CGTTTTACTGTGCATGTCTTACTACTTTTGACCGCGATGATGTGCTTTTGAAGAACTTTGC	265	
Db	256	CGTTTTACTGTGCATGTCTTACTACTTTTGACCGCGATGATGTGCTTTTGAAGAACTTTGC	315	
Qy	266	CAAAATCTTTTCTTCACCAACTCTCATGAGGAGGGAACATGCTCAGAAACTGATGAAGCT	325	
Db	316	CAAAATCTTTTCTTCACCAACTCTCATGAGGAGGGAACATGCTCAGAAACTGATGAAGCT	375	
Qy	326	GCAGAACCAACGAGGTGCGCGAAATCTTCTTTCAGGATATCAAGAAACCAGACTGTGTATGA	385	
Db	376	GCAGAACCAACGAGGTGCGCGAAATCTTCTTTCAGGATATCAAGAAACCAGACTGTGTATGA	435	
Qy	386	CTGGGAGAGCGGGCTGAATGCAATGGAGTGTGCATTACATTTGGAAAAAAATGTGAATCA	445	

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Db      436  CTGGGAGCGGGCTGAATGCAATGGAATGTGCATTGCAATTTGGAAAAAATGTGAATCA 495
Qy      446  GTCACACTACTGGAATTC 462
          |||||
Db      496  GTCACACTACTGGAAC 512
          |||||

RESULT 11
US-09-919-580-912
; Sequence 912, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 912
; LENGTH: 791
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 628, 662, 677, 703, 715, 741, 785, 786
; OTHER INFORMATION: n = A,T,C or G
US-09-919-580-912

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Query Match	41.9%;	Score 373.4;	DB 9;	Length 791;
Best Local Similarity	99.7%;	Pred. No. 2.6e-110;		
Matches 374;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	86	CCGCCTCTCTTAGTCGCGCCATGACGACCGCTCCACCTCGACGCTCGAGGTGCGCCAGAACTA	145	
Db	180	CGGGCTCTCTTAGTCGCGCCATGACGACCGCTCCACCTCGAGGTGCGCCAGAACTA	239	
Qy	146	CCACCGAGTCTCAGAGCGCGCCATCAACCGCCAGATCAACTGGAGCTCTACGCTCTCTTA	205	
Db	240	CCACCGAGTCTCAGAGCGCGCCATCAACCGCCAGATCAACTGGAGCTCTACGCTCTCTTA	299	
Qy	206	CGTTTACTGTCCATGTCTTACTACTTTGACCGCGATGATGTGCTTTTGAGAACTTTGC	265	
Db	300	CGTTTACTGTCCATGTCTTACTACTTTGACCGCGATGATGTGCTTTTGAGAACTTTGC	359	
Qy	266	CAAAATCTTTCTTCCACCAATCTCATGAGGAGGGAAACATCTCAGAAACTGATGAAGCT	325	
Db	360	CAAAATCTTTCTTCCACCAATCTCATGAGGAGGGAAACATCTCAGAAACTGATGAAGCT	419	
Qy	326	GCAGAACCAACGAGGTGGCGAAATCTTCTTTCAGGATATCAAGAAACACAGACTGTGATGA	385	
Db	420	GCAGAACCAACGAGGTGGCGAAATCTTCTTTCAGGATATCAAGAAACACAGACTGTGATGA	479	
Qy	386	CTGGGAGCGGGCTGAAATGCAATGGAGGTGTCATTTCATTTGGAAAAAAATGTCAATCA	445	
Db	480	CTGGGAGCGGGCTGAAATGCAATGGAGGTGTCATTTCATTTGGAAAAAAATGTCAATCA	539	
Qy	446	GTCACTACTGGAATT	460	
Db	540	GTCACTACTGGAAT	554	

## RESULT 12

RESUMI 12  
US-09-880-107-2174  
; Sequence 2174. Application US/09880107  
; Patent No. US20020142981A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, Darci T.  
; APPLICANT: Vockley, Joseph G.  
; APPLICANT: Scherr, Uwe

```
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2174
; LENGTH: 1198
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 L20941
US-09-880-107-2174

Query Match 41.9%; Score 373; DB 9; Length 1198;
Best Local Similarity 98.7%; Pred. No. 4.5e-110;
Matches 376; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 82 CAGCGCGCTCTCTTAGTGGCGGCATGACGACCGCGTCCACCTCGCAGGTCGCCAGA 141
Db 183 CCGCGCGCTCTCTTAGTGGCGGCATGACGACCGCGTCCACCTCGCAGGTCGCCAGA 242

QY 142 ACTACACAGGACTCAGAGGCGGCATCAACCGCCAGATCAACTGGAGCTTACGCCT 201
Db 243 ACTACACAGGACTCAGAGGCGGCATCAACCGCCAGATCAACTGGAGCTTACGCCT 302

QY 202 CCTAGCTTACCTGTCCTTAGTCTTACTACTTTGACCGCGATGATGGCTTTGAAGAAT 261
Db 303 CCTAGCTTACCTGTCCTTAGTCTTACTACTTTGACCGCGATGATGGCTTTGAAGAAT 362

QY 262 TTGCCAAATACCTTCTTCCAAATCTCATGAGGAGGGAACATGCTGAGAACTGATGA 321
Db 363 TTGCCAAATACCTTCTTCCAAATCTCATGAGGAGGGAACATGCTGAGAACTGATGA 422

QY 322 AGCTCAGAACCAACGAGGTGCGCAATCTTCTTCCAGATATCAAGAAACGAGCTGTG 381
Db 423 AGCTCAGAACCAACGAGGTGCGCAATCTTCTTCCAGATATCAAGAAACGAGCTGTG 482

QY 382 ATGACTGGGAGCGCGGTGAATGCAATGAGTGTGCATTACATTTGAAAAAATGTGA 441
Db 483 ATGACTGGGAGCGCGGTGAATGCAATGAGTGTGCATTACATTTGAAAAAATGTGA 542

QY 442 ATCAGTCACTACTGGAATTC 462
Db 543 ATCAGTCACTACTGGAATTC 563

RESULT 13
US-10-425-115-12412
; Sequence 12412, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yihua
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 12412
; LENGTH: 882
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure

; LOCATION: (1)..(882)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_1111315C.1
US-10-425-115-12412

Query Match 41.8%; Score 372.8; DB 18; Length 882;
Best Local Similarity 99.2%; Pred. No. 4.4e-110;
Matches 374; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 86 CCGCTCTCTCTTAGTGGCGGCATGACGACCGCGTCCACCTCGCAGGTCGCCAGAATA 145
Db 173 CCGCTCTCTCTTAGTGGCGGCATGACGACCGCGTCCACCTCGCAGGTCGCCAGAATA 232

QY 146 CCACGAGACTCAGAGGCGGCATCAACCGCCAGATCAACTGGAGCTCTACGCCCTCTA 205
Db 233 CCACGAGACTCAGAGGCGGCATCAACCGCCAGATCAACTGGAGCTCTACGCCCTCTA 292

QY 206 CGTTTACCTGTCCTTAGTCTTACTACTTTTGAACCGGATGATGGCTTTGAAGAATTTTC 265
Db 293 CGTTTACCTGTCCTTAGTCTTACTACTTTTGAACCGGATGATGGCTTTGAAGAATTTTC 352

QY 266 CAAATACCTTCTTCCAAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 325
Db 353 CAAATACCTTCTTCCAAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 412

QY 326 GCAGAACCAACGAGGTGCGCAATCTTCTTCCAGATATCAAGAAACGAGCTGTGATGA 385
Db 413 GCAGAACCAACGAGGTGCGCAATCTTCTTCCAGATATCAAGAAACGAGCTGTGATGA 472

QY 386 CTGGGAGAGCGCGGTGAATGCAATGAGTGTGCATTACATTTGAAAAAATGTGAATCA 445
Db 473 CTGGGAGAGCGCGGTGAATGCAATGAGTGTGCATTACATTTGAAAAAATGTGAATCA 532

QY 446 GTCACTACTGGAATTC 462
Db 533 GTCACTACTGGAATTC 549

RESULT 14
US-09-919-580-889
; Sequence 889, Application US/09919580
; Patent No. US20020110832A1
; GENERAL INFORMATION:
; APPLICANT: Pyle, Ruth
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.552
; CURRENT APPLICATION NUMBER: US/09/919,580
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 889
; LENGTH: 776
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 675, 690, 711, 718, 742, 759
; OTHER INFORMATION: n = A,T,C or G
US-09-919-580-889

Query Match 41.8%; Score 372.2; DB 9; Length 776;
Best Local Similarity 99.2%; Pred. No. 6.4e-110;
Matches 374; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 86 CCGCTCTCTCTTAGTGGCGGCATGACGACCGCGTCCACCTCGCAGGTCGCCAGAATA 145
Db 178 CCGCTCTCTCTTAGTGGCGGCATGACGACCGCGTCCACCTCGCAGGTCGCCAGAATA 237

QY 146 CCACGAGACTCAGAGGCGGCATCAACCGCCAGATCAACTGGAGCTCTACGCCCTCTA 205
```

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Db 238 CCACGAGACTCAGAGGGCGGCATCAACGCCAGATCAACCTGGAGCTCTACGCCTCCTA 297
Qy 206 GCTTTACCTGTCATGCTTACTACTTTGACCGCATGATGGCTTTTGAAGAACTTTGC 265
Db 298 GCTTTACCTGTCATGCTTACTACTTTGACCGCATGATGGCTTTGAGAACTTTGC 357
Qy 266 CAATATCTTTCTTACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 325
Db 358 CAATATCTTTCTTACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 417
Qy 326 GCAGAACCAACGAGGTGGCGCAATCTTCTTCAGGATATCAAGAAACAGACTGTGATGA 385
Db 418 GCAGAACCAACGAGGTGGCGCAATCTTCTTCAGGATATCAAGAAACAGACTGTGATGA 477
Qy 386 CTGGGAGAGCGGGCTGAAATGCAATGGAGTGTGCATTACATTTGGAAAAAAATGTGAATCA 445
Db 478 CTGGGAGAGCGGGCTGAAATGCAATGGAGTGTGCATTACATTTGGAAAAAAATGTGAATCA 537
Qy 446 GTCACACTGGAATTC 462
Db 538 GTCACACTGGAATTC 554
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## RESULT 15

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US-09-823-245A-42
; Sequence 42, Application US/09823245A
; Publication No. US20020039760A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6401
; CURRENT APPLICATION NUMBER: US/09/823,245A
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/194,941
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 631
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 900
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-823-245A-42
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Query Match 41.8%; Score 372.2; DB 9; Length 900;
Best Local Similarity 99.2%; Pred No. 7e-110;
Matches 374; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 86 CGGCTCTCTTAGTGGCGGCATGACGACCGCGTCCACTCGCAGGTGGCCAGAACTA 145
Db 166 CGGCTCTCTTAGTGGCGGCATGACGACCGCGTCCACTCGCAGGTGGCCAGAACTA 225
Qy 146 CCACGAGACTCAGAGGGCGGCATCAACGCCAGATCAACCTGGAGCTCTAGCCCTCCTA 205
Db 226 CCACGAGACTCAGAGGGCGGCATCAACGCCAGATCAACCTGGAGCTCTAGCCCTCCTA 285
Qy 206 GCTTTACCTGTCATGCTTACTACTTTGACCGCATGATGGCTTTGAAGAACTTTGC 265
Db 286 GCTTTACCTGTCATGCTTACTACTTTGACCGCATGATGGCTTTGAAGAACTTTGC 345
Qy 266 CAATATCTTTCTTACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 325
Db 346 CAATATCTTTCTTACCAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 405
Qy 326 GCAGAACCAACGAGGTGGCGCAATCTTCTTCAGGATATCAAGAAACAGACTGTGATGA 385
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Db 406 GCAGAACCAACGAGGTGGCGCAATCTTCTTCAGGATATCAAGAAACAGACTGTGATGA 465
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Db 466 CTGGGAGAGCGGGCTGAAATGCAATGGAGTGTGCATTACATTTGGAAAAAAATGTGAATCA 525
Qy 446 GTCACACTGGAATTC 462
Db 526 GTCACACTGGAATTC 542
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Search completed: April 1, 2005, 13:16:57  
Job time : 438 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 1, 2005, 11:27:22 ; Search time 2388 Seconds

(without alignments)  
14202.372 Million cell updates/sec

Title: US-09-786-867C-1

Perfect score: 891

Sequence: 1 ttgacaccagaccactggct.....acgacaacataaaaaaa 891

Scoring table: IDENTITY\_NUC

GAP 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hic:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gssi:\*

9: gb\_gse2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	375.8	42.2	688	BG542331	BG542331 602571887
2	375.8	42.2	803	BU955418	BU955418 AGENCOURT
3	375.8	42.2	877	BU170044	BU170044 AGENCOURT
4	375	42.1	602	BI544288	BI544288 603241665
5	375	42.1	704	BE281505	BE281505 601155067
6	375	42.1	900	BE308934	BE308934 601497872
7	375	42.1	978	BE562266	BE562266 601344724
8	374.8	42.1	1001	BU196441	BU196441 AGENCOURT
9	374.6	42.0	575	BU073943	BU073943 in26e12.y
10	374.6	42.0	788	BG163468	BG163468 602338464
11	374.6	42.0	875	BF983589	BF983589 602306579
12	374.6	42.0	942	BE740697	BE740697 601593667
13	374.6	42.0	953	BF976359	BF976359 602244490
14	374.2	42.0	507	BQ637251	BQ637251 he07f05.y
15	374.2	42.0	579	BP214869	BP214869 BP214869
16	374.2	42.0	582	BP214989	BP214989 BP214989
17	374.2	42.0	582	BP228811	BP228811 BP228811
18	374.2	42.0	582	BP353301	BP353301 BP353301
19	374.2	42.0	583	BP295488	BP295488 BP295488
20	374.2	42.0	642	CF128424	CF128424 UI-HF-ET0
21	374.2	42.0	697	CF128432	CF128432 UI-HF-ET0
22	374.2	42.0	726	CF131121	CF131121 UI-HF-ET0
23	374.2	42.0	772	CF131109	CF131109 UI-HF-ET0
24	374.2	42.0	773	BQ219393	BQ219393 AGENCOURT

25	374.2	42.0	817	2	BF576393	BF576393 602134292
26	374.2	42.0	952	4	BG331712	BG331712 602433128
27	374	42.0	567	5	BP234849	BP234849 BP234849
28	374	42.0	582	5	BP229326	BP229326 BP229326
29	374	42.0	582	5	BP231281	BP231281 BP231281
30	374	42.0	582	5	BP315816	BP315816 BP315816
31	374	42.0	582	5	BP352853	BP352853 BP352853
32	374	42.0	583	5	BP214599	BP214599 BP214599
33	374	42.0	583	5	BP231792	BP231792 BP231792
34	373.8	42.0	430	5	BQ638826	BQ638826 hd28b01.y
35	373.8	42.0	456	5	BP232703	BP232703 BP232703
36	373.8	42.0	458	4	BM686184	BM686184 UI-E-CR0-
37	373.8	42.0	461	5	BQ316932	BQ316932 CM0-CT034
38	373.8	42.0	484	1	AJ705380	AJ705380 AJ705380
39	373.8	42.0	484	5	BP234848	BP234848 BP234848
40	373.8	42.0	485	6	CB751823	CB751823 TGESTZYHS
41	373.8	42.0	485	7	NS2504	NS2504 YV52a11.s1
42	373.8	42.0	497	2	BF724302	BF724302 bx03c06.y
43	373.8	42.0	508	2	BF727248	BF727248 by18h05.y
44	373.8	42.0	515	5	BM887644	BM887644 TM231 Hum
45	373.8	42.0	517	4	BM798732	BM798732 K-EST0082

## ALIGNMENTS

RESULT 1  
BG542331  
LOCUS  
DEFINITION BG542331 688 bp mRNA linear EST 03-APR-2001  
602571887F1 NIH\_MGC\_77 Homo sapiens cdna clone IMAGE:4696508 5',  
mRNA sequence.  
ACCESSION BG542331  
VERSION BG542331.1 GI:13534564  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 688)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE  
JOURNAL  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCM1523 row: m column: 21  
High quality sequence stop: 679.  
Location/Qualifiers  
1..688  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4696508"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NIH\_MGC\_77"  
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1: sfii (ggccattggcc); Site 2: sfii (ggccattggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGCG-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGCGGCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 Kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

ORIGIN



Plate: LLAM13194 row: k column: 04

High quality sequence stop: 643.

# FEATURES

source

Location/Qualifiers

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1. .877
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6008955"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_68"
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.8 kb. Library constructed by Life
Technologies."
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## ORIGIN

```
Query Match 42.2%; Score 375.8; DB 5; Length 877;
Best Local Similarity 97.0%; Pred. No. 4.1e-98;
Matches 383; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 68 CACTCCATTGCATTCAGCCGCTCTCTTAGTCGCGCCATGACGACCGGTCCACCTC 127
Db 73 CCTCCGTCACTCTTACCGCTCTCTTAGTCGCGCCATGACGACCGGTCCACCTC 132

QY 128 CGAGTGGCCAGAACTACCAACAGACTCAGAGCGCCATCAACCGCAGATCAACT 187
Db 133 CGAGTGGCCAGAACTACCAACAGACTCAGAGCGCCATCAACCGCAGATCAACT 192

QY 188 GGAGCTCTACGCTCTCTAGTTTACCTGTTCATGCTTACTACTTTGACCGGATGAT 247
Db 193 GGAGCTCTACGCTCTCTAGTTTACCTGTTCATGCTTACTACTTTGACCGGATGAT 252

QY 248 GGCCTTGAAGAACTTTGCAATACTTTTCCACCAATCTCATGAGGAGGGAACATGC 307
Db 253 GGCCTTGAAGAACTTTGCAATACTTTTCCACCAATCTCATGAGGAGGGAACATGC 312

QY 308 TGAGAACTGATGAAGCTGCAGAACCAAGAGGTGGCGAATCTTCTTTCAGGATATCAA 367
Db 313 TGAGAACTGATGAAGCTGCAGAACCAAGAGGTGGCGAATCTTCTTTCAGGATATCAA 372

QY 368 GAAACACAGCTGTGATGATCTGGAGAGCGGCTGAATCAATGAGTGTGCATTACATTT 427
Db 373 GAAACACAGCTGTGATGATCTGGAGAGCGGCTGAATCAATGAGTGTGCATTACATTT 432

QY 428 GGAAAAAATGTGAATCACTACTACTGGAATTC 462
Db 433 GGAAAAAATGTGAATCACTACTACTGGAATTC 467
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## RESULT 4

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BI544288
LOCUS 603241665F1 NIH_MGC_95 602 bp mRNA linear EST 05-SEP-2001
DEFINITION 603241665F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5284120 5',
mRNA sequence.
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## ACCESSION

BI544288

## VERSION

BI544288.1 GI:15431600

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 602)  
NIH-MGC <http://mgi.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs@mail.nih.gov](mailto:cgapbs@mail.nih.gov)  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
cDNA Library preparation: Michael J. Brownstein (NHGRI), Shiraki  
Tohiyuki and Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

Plate: LLAM11718 row: a column: 17

High quality sequence stop: 600.

# FEATURES

source

Location/Qualifiers

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1. .602
/organism="Homo sapiens"
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/clone="IMAGE:5284120"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_95"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gtcgag); Oligo-dt primed using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.5 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this
is a NIH_MGC Library."
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## ORIGIN

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Query Match 42.1%; Score 375; DB 4; Length 602;
Best Local Similarity 97.4%; Pred. No. 6.4e-98;
Matches 381; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 72 CCATTGATTCAGCCGCTCTCTTAGTCGCGCCATGACGACCGGTCCACCTCGCAG 131
Db 174 CCACGCGCGCGCGCTCTCTTAGTCGCGCCATGACGACCGGTCCACCTCGCAG 233

QY 132 GTGCGCCAGAACTACCAACAGACTCAGAGCGCCATCAACCGCAGATCAACCTGGAG 191
Db 234 GTGCGCCAGAACTACCAACAGACTCAGAGCGCCATCAACCGCAGATCAACCTGGAG 293

QY 192 CTCTAGCGCTCTAGTTTACCTGTTCATGCTTACTACTTTGACCGGATGATGGCT 251
Db 294 CTCTAGCGCTCTAGTTTACCTGTTCATGCTTACTACTTTGACCGGATGATGGCT 353

QY 252 TTGAAGAACTTTGCCAATACTTTTCCACCAATCTCATGAGGAGGGAACATCTGAG 311
Db 354 TTGAAGAACTTTGCCAATACTTTTCCACCAATCTCATGAGGAGGGAACATCTGAG 413

QY 312 AAACCTGATGAAGCTGCAGAACCAACGAGGTGGCGAATCTTCTTTCAGGATATCAAGAA 371
Db 414 AAACCTGATGAAGCTGCAGAACCAACGAGGTGGCGAATCTTCTTTCAGGATATCAAGAA 473

QY 372 CCAGACTGTGATGATGGAGAGCGGCTGAATGCAATGGAGTGTGCATTACATTTGGA 431
Db 474 CCAGACTGTGATGATGGAGAGCGGCTGAATGCAATGGAGTGTGCATTACATTTGGA 533

QY 432 AAAAATGTAATCAGTCACTACTGGAATTC 462
Db 534 AAAAATGTAATCAGTCACTACTGGAATTC 564
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## RESULT 5

### BE281505

### LOCUS

601155067F1 NIH\_MGC\_21 704 bp mRNA linear EST 13-JUL-2000

### DEFINITION

601155067F1 NIH\_MGC\_21 Homo sapiens cDNA clone IMAGE:3138449 5',  
mRNA sequence.

### ACCESSION

BE281505

### VERSION

BE281505.1 GI:9156525

### KEYWORDS

EST.

### SOURCE

Homo sapiens (human)

### ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 704)  
NIH-MGC <http://mgi.nci.nih.gov/>.

**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**COMMENT** Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
Plate: LLCMI03 row: f column: 18  
High quality sequence stop: 655.

**FEATURES**  
**source**

## ORIGIN

Query Match	42.1%	Score	375;	DB 2;	Length	704;			
Best Local Similarity	97.4%;	Pred. No.	6.6e-98;						
Matches	381;	Conservative	0;	Mismatches	10;	Indels	0;	Gaps	0;
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QY	132	GTGCGCCAGAACTACCAACGAGACTCAGAGCGCGCCATCAACGCCAGATCAACCTGGAG	191						
DB	180	GTGCGCCAGAACTACCAACGAGACTCAGAGCGCGCCATCAACGCCAGATCAACCTGGAG	239						
QY	192	CTCTAGCGCTCTTACGTTTACCTGTCCATGCTTACTACTTTACGCGCATGATGGCT	251						
DB	240	CTCTAGCGCTCTTACGTTTACCTGTCCATGCTTACTACTTTACGCGCATGATGGCT	299						
QY	252	TTGAAGAACTTTGCCAAATACTTTCTTCAACAACTCTCATGAGGAGGGGAACATGCTGAG	311						
DB	300	TTGAAGAACTTTGCCAAATACTTTCTTCAACAACTCTCATGAGGAGGGGAACATGCTGAG	359						
QY	312	AAACTGATGAAGCTGCAGAAACCAACGAGGTGGCGCGAATCTTCTTTCAGGATATCAAGAAA	371						
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DB	420	CCAGA CTGTGATGACTGGGAGAGCGGCTGAATGCAATGGAGTGTGCATTACATTGGAA	479						
QY	432	AAAAATGTGAATCAGTCACCTACTTGGAAATTC	462						
DB	480	AAAAATGTGAATCAGTCACCTACTTGGAACTGC	510						

[illegible]

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KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
cdna Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LNCM353 row: o column: 06
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High quality sequence stop: 812.
Location/Qualifiers
1..978
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:367789"
/tissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 8"
/Note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

FEATURES
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/clone="IMAGE:367789"
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/Note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN
Query Match 42.1%; Score 375; DB 2; Length 978;
Best Local Similarity 97.4%; Pred. No. 7.3e-98;
Matches 381; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 72 CCATTGCTTACCGCGCTCTCTTAGTCGGCGCATGACGACCGCTCCACCTCGCAG 131
DB 182 CCACCGCGCGCGCGCTCTCTTAGTCGGCGCATGACGACCGCTCCACCTCGCAG 241
QY 132 GTGCGCCAGAACTACCAACGAGCTCAGAGCGCGCATCAACCGCGCATCAACCTGGAG 191
DB 242 GTGCGCCAGAACTACCAACGAGCTCAGAGCGCGCATCAACCGCGCATCAACCTGGAG 301
QY 192 CTCTACGCTCTACGTTTACCTGTCATGTCCTTACTACTTTGACCGCATGATGGCT 251
DB 302 CTCTACGCTCTACGTTTACCTGTCATGTCCTTACTACTTTGACCGCATGATGGCT 361
QY 252 TTGAGAACTTTGCCAAATCTTTCTTACCAATCTCATGAGAGAGGAACTGAG 311
DB 362 TTGAGAACTTTGCCAAATCTTTCTTACCAATCTCATGAGAGAGGAACTGAG 421
QY 312 AAATGATGAAGCTGCAGAACCAACGAGGTGGCGCAATCTTCTTCAAGATCAAGAA 371
DB 422 AAATGATGAAGCTGCAGAACCAACGAGGTGGCGCAATCTTCTTCAAGATCAAGAA 481
QY 372 CCAGACTGTGATGCTGGAGAGCGGCTGAATGCAATGGAGTGTGCATTATTTGAA 431
DB 482 CCAGACTGTGATGCTGGAGAGCGGCTGAATGCAATGGAGTGTGCATTATTTGAA 541
QY 432 AAAATGTGAATCAGTCACTACTGGAATTC 462
DB 542 AAAATGTGAATCAGTCACTACTGGAATTC 572

RESULT 8

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BUI96441
LOCUS BUI96441 1001 bp mRNA linear EST 04-SEP-2002
DEFINITION AGENCOURT_8102329 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6252597
5', mRNA sequence.
ACCESSION BUI96441
VERSION BUI96441.1 GI:22710412
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTP/DTF
cdna Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LNCM2399 row: b column: 22
High quality sequence start: 20
High quality sequence stop: 467.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:6252597"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 112"
/Note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dt priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN
Query Match 42.1%; Score 374.8; DB 5; Length 1001;
Best Local Similarity 99.5%; Pred. No. 8.4e-98;
Matches 376; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 86 CGGCTCTCTTAGTCGGCGCATGACGACCGCTCCACCTCGAGGTGCGCCAGAACTA 145
DB 205 CGGCTCTCTTAGTCGGCGCATGACGACCGCTCCACCTCGAGGTGCGCCAGAACTA 264
QY 146 CCACGAGACTCAGAGCGCGCATCAACCGCGCATCAACCTGGAGTCTAGCCCTCTTA 205
DB 265 CCACGAGACTCAGAGCGCGCATCAACCGCGCATCAACCTGGAGTCTAGCCCTCTTA 324
QY 206 CGTTTACCTGCTCCATGCTTACTACTTTGACCGCATGATGGCTTTGAAGAACTTTGC 265
DB 325 CGTTTACCTGCTCCATGCTTACTACTTTGACCGCATGATGGCTTTGAAGAACTTTGC 384
QY 266 CAATATCTTTCTTACCAATCTCATGAGAGAGGAAATGCTGAGAACTGATGAAGCT 325
DB 385 CAATATCTTTCTTACCAATCTCATGAGAGAGGAAATGCTGAGAACTGATGAAGCT 444
QY 326 CGAGAACCAACGAGGTGGCGCAATCTTCTTCAAGATATCAAGAACCAAGCTGTGATCA 385
DB 445 CGAGAACCAACGAGGTGGCGCAATCTTCTTCAAGATATCAAGAACCAAGCTGTGATCA 504
QY 386 CTGGGAGAGCGGCTGAATGCAATGGAGTGTGCATTACATTTGGAAAAAATGTGAATCA 445
DB 505 CTGGGAGAGCGGCTGAATGCAATGGAGTGTGCATTACATTTGGAAAAAATGTGAATCA 564

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QY 446 GTCACCTACTGGAATTCCTCC 463
DB 565 GTCACCTACTGGAATTCCTCC 582

RESULT 9
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LOCUS in26e12.y1 Human Fetal Pancreas 1B Homo sapiens cDNA clone IMAGE:
DEFINITION 5' similar to SW:FRH_HUMAN P027914 FERRITIN HEAVY CHAIN ;, mRNA
sequence.
ACCESSION BU073943
VERSION BU073943.1 GI:22515132
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@imgate.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 447.
Location/Qualifiers
1. .575
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:"
/tissue_type="Fetal Pancreas (4 Pooled Donors, 18 - 20
weeks, Stratagene #738023)"
/dev_stages="Fetal Pancreas"
/clone_lib="Human Fetal Pancreas 1B"
/note="Vector: pBluescript SK(-); Site 1: NotI; Site 2:
XhoI; cDNA made by oligo-dT priming. Size-selected on
agarose gel. Average insert size ~1kb. 5' XhoI site was
destroyed after directional cloning. Amplified once.
Contact information: Hiroshi Inoue, MD, Metabolism Div.
(Alan Permutt Lab), Washington University School of
Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO
63110 E-mail: hinoue@imgate.wustl.edu Tel: 314-362-1916,
Fax: 314-747-2692."

ORIGIN
Query Match 42.0%; Score 374.6; DB 5; Length 575;
Best Local Similarity 99.0%; Pred. No. 8.2e-98; Mismatches 4; Indels 0; Gaps 0;
Matches 377; Conservative 0;

QY 82 CAGCCCGCCTCTCTTAGTCGCGCCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGA 141
DB 10 CCGGCCGCTCTCTTAGTCGCGCCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGA 69

QY 142 ACTACACAGGACTCAGAGGCGCCATCAACGCCAGATCAACTGGAGCTCTAGCCT 201
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DB 70 ACTACACAGGACTCAGAGGCGCCATCAACGCCAGATCAACCTGGAGCTCTACGCCT 129
QY 202 CTTACGTTTACCTGTCATGCTTACTACTTTTACCGCGGATGATGGCTTTGAAGAACT 261
DB 130 CTTACGTTTACCTGTCATGCTTACTACTTTTACCGCGGATGATGGCTTTGAAGAACT 189
QY 262 TTGCCAAATATCTTTCTTCCAAATCTCATGAGGAGGGAACATGCTGAGAAAATGATGA 321
DB 190 TTGCCAAATATCTTTCTTCCAAATCTCATGAGGAGGGAACATGCTGAGAAAATGATGA 249
QY 322 AGCTGAGAAACCAACGAGGTGGCGGAATCTTCTTACGATATCAAGAAACCAAGACTGTG 381
DB 250 AGCTGAGAAACCAACGAGGTGGCGGAATCTTCTTACGATATCAAGAAACCAAGACTGTG 309
QY 382 ATGACTGGGAGAGCGGCTGAATGCAATGAGTGTGCATTACATTTGAAAAAATGATGA 441
DB 310 ATGACTGGGAGAGCGGCTGAATGCAATGAGTGTGCATTACATTTGAAAAAATGATGA 369
QY 442 ATCAGTCACTACTGGAATTCCT 462
DB 370 ATCAGTCACTACTGGAATTCCT 390

RESULT 10
BU073943
LOCUS 602338464P1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4446591 5',
DEFINITION mRNA sequence.
ACCESSION BU073943
VERSION BU073943.1 GI:12670171
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@ps-research.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM10225 row: p column: 16
High quality sequence stop: 754.
Location/Qualifiers
1. .788
/organism="Homo sapiens"
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/clone_lib="NIH_MGC 89"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN
Query Match 42.0%; Score 374.6; DB 4; Length 788;
Best Local Similarity 99.0%; Pred. No. 9e-98; Mismatches 4; Indels 0; Gaps 0;
Matches 377; Conservative 0;

QY 82 CAGCCCGCCTCTCTTAGTCGCGCCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGA 141
DB 150 CCGGCCGCTCTCTTAGTCGCGCCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGA 209

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Query Match 42.0%; Score 374.6; DB 2; Length 942;  
 Best Local Similarity 99.0%; Pred. No. 9.4e-98;  
 Matches 377; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 82 GAGCGCGCTCTCCTTAGTCGCGCGCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGA 141  
 DB 118 CCGCGCGCTCTCCTTAGTCGCGCGCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGA 177  
 QY 142 ACTACACGAGACTCAGAGGCGCGCATCAACCGCAGATCAACCTGGAGCTCTACGCT 201  
 DB 178 ACTACACGAGACTCAGAGGCGCGCATCAACCGCAGATCAACCTGGAGCTCTACGCT 237  
 QY 202 CTTAGTTTACCTGTCCTTACTTACTTCTTACCTTGGCGGATGATGGCTTTGAAGAAGT 261  
 DB 238 CTTAGTTTACCTGTCCTTACTTACTTGGCGGATGATGGCTTTGAAGAAGT 297  
 QY 262 TTGCCAAATACCTTCTTACCAATCTCATGAGGAGGAGGAACTGCTGAGAACTGATGA 321  
 DB 298 TTGCCAAATACCTTCTTACCAATCTCATGAGGAGGAGGAACTGCTGAGAACTGATGA 357  
 QY 322 AGCTGAGAACCAAGAGGTGCGCAATCTTCTTACGATATCAAGAAACCGAGACTGTG 381  
 DB 358 AGCTGAGAACCAAGAGGTGCGCAATCTTCTTACGATATCAAGAAACCGAGACTGTG 417  
 QY 382 ATGACTGGAGAGCGGGCTGAATCAATGGAGTGTGCTTACATTTGGAAAAAATGTGA 441  
 DB 418 ATGACTGGAGAGCGGGCTGAATCAATGGAGTGTGCTTACATTTGGAAAAAATGTGA 477  
 QY 442 ATCACTCACTACTGGAATTC 462  
 DB 478 ATCACTCACTACTGGAATTC 498

RESULT 13  
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 LOCUS 602244490F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4395334 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BF976359  
 VERSION BF976359.1 GI:12343676  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 953)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLC61206 row: d column: 23  
 High quality sequence stop: 716.  
 Location/Qualifiers  
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 /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;  
 Site 2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the

FEATURES  
 source

following 5' adaptor: GGCACGAG(G). Size-selected >500bp  
 for average insert size 1.8kb. Library constructed by Ling  
 Hong in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 42.0%; Score 374.6; DB 4; Length 953;  
 Best Local Similarity 99.0%; Pred. No. 9.5e-98;  
 Matches 377; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 82 CAGCGCGCTCTCCTTAGTCGCGCGCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGA 141  
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 QY 142 ACTACACGAGACTCAGAGGCGCGCATCAACCGCAGATCAACCTGAGCTCTACGCT 201  
 DB 227 ACTACACGAGACTCAGAGGCGCGCATCAACCGCAGATCAACCTGAGCTCTACGCT 286  
 QY 202 CTTAGTTTACCTGTCCTTACTTACTTCTTACCTTGGCGGATGATGGCTTTGAAGAAGT 261  
 DB 287 CTTAGTTTACCTGTCCTTACTTACTTGGCGGATGATGGCTTTGAAGAAGT 346  
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 DB 347 TTGCCAAATACCTTCTTACCAATCTCATGAGGAGGAGGAACTGCTGAGAACTGATGA 406  
 QY 322 AGCTGAGAACCAAGAGGTGCGCAATCTTCTTACGATATCAAGAAACCGAGACTGTG 381  
 DB 407 AGCTGAGAACCAAGAGGTGCGCAATCTTCTTACGATATCAAGAAACCGAGACTGTG 466  
 QY 382 ATGACTGGAGAGCGGGCTGAATCAATGGAGTGTGCTTACATTTGGAAAAAATGTGA 441  
 DB 467 ATGACTGGAGAGCGGGCTGAATCAATGGAGTGTGCTTACATTTGGAAAAAATGTGA 526  
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 DB 527 ATCACTCACTACTGGAATTC 547

RESULT 14  
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 DEFINITION he07f05.y1 Human Retina cDNA (Un-normalized, unamplified): hd/he  
 Homo sapiens cDNA clone he07f05 5', mRNA sequence.  
 ACCESSION BF976359  
 VERSION BF976359.1 GI:21761710  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 507)  
 AUTHORS Wistow, G., Bernstein, S.L., Wyatt, M.K., Ray, S., Behal, A.,  
 Touchman, J.W., Bouffard, G., Smith, D., and Peterson, K.  
 TITLE Expressed sequence tag analysis of human retina for the NEIBank  
 Project: Rebinding, an abundant, novel retinal cDNA and alternative  
 splicing of other retina-preferred gene transcripts  
 JOURNAL Mol. Vis. 8 (4), 196-204 (2002)  
 MEDLINE 22103461  
 PUBMED 12107411  
 COMMENT Contact: Wistow G  
 Section on Molecular Structure and Function  
 National Eye Institute  
 6/331, NIH, Bethesda, MD 20892-2740, USA  
 Tel: 301 402 3452  
 Fax: 301 496 0078  
 Email: [graeame@helix.nih.gov](mailto:graeame@helix.nih.gov)  
 Plate: 07 row: f column: 05  
 Seq primer: M13Rpl reverse primer (ABI).  
 Location/Qualifiers  
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 unamplified): hd/he"  
 /note="Organ: Eye; Vector: pSPORT1; Neural retina tissue  
 was dissected from two 80 year old donors with no observed  
 eye disease. 100ug of total RNA was used for library  
 construction. A directionally cloned cDNA library in the  
 pSPORT1 vector (Life Technologies) was constructed at  
 Bioserve Biotechnology (Laurel MD) essentially following  
 the protocols of the SuperScript Plasmid System full  
 details of which are contained in the manufacturer's  
 instruction manual (<http://www.lifetech.com/>). First  
 strand synthesis was carried out using a Not I  
 primer-adaptor  
 15'-GGACTGATCTAGATCGGAGCGCGCC(T)15-3'. EST analysis  
 was performed on the unamplified library at the NIH  
 Intramural Sequencing Center (NISC)."  
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## ORIGIN

Query Match 42.0%; Score 374.2; DB 5; Length 507;  
 Best Local Similarity 96.7%; Pred. No. 1e-97;  
 Matches 382; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
 QY 68 CACTCATTGCAATTCAGCGCGCTCTCTTCTAGTCGGCGCATGACGCGGTCCACCTC 127  
 DB 44 CGCTGTTCCACCGCGCGCTCTCTTCTAGTCGGCGCATGACGCGGTCCACCTC 103  
 QY 128 CGAGTGGCCGAGAACTACACAGGACTCAGAGCGCGCATCAACCGCAGATCAACT 187  
 DB 104 GCAGTGGCCGAGAACTACACAGGACTCAGAGCGCGCATCAACCGCAGATCAACT 163  
 QY 188 GGAGCTCTACGCTCTAGCTTACTGTCATGCTTACTACTTTGACCGCGATGATG 247  
 DB 164 GGAGCTCTACGCTCTAGCTTACTGTCATGCTTACTACTTTGACCGCGATGATG 223  
 QY 248 GCTTTGAGAACTTTGCCAAATCTCTTCCAACTCTCATGAGGAGGGAACATGC 307  
 DB 224 GCTTTGAGAACTTTGCCAAATCTCTTCCAACTCTCATGAGGAGGGAACATGC 283  
 QY 308 TGAGAACTGATGAAGCTGCAGAACCAACGAGGTGGCGGAATCTTCTTCAGGATATCAA 367  
 DB 284 TGAGAACTGATGAAGCTGCAGAACCAACGAGGTGGCGGAATCTTCTTCAGGATATCAA 343  
 QY 368 GAAACAGACTGTGATGACTGGAGAGCGGCTGATGCAATGGAGTGTGCATTACATTT 427  
 DB 344 GAAACAGACTGTGATGACTGGAGAGCGGCTGATGCAATGGAGTGTGCATTACATTT 403  
 QY 428 GGAAAAAATGTAATCACTCACTACTGGAATTC 462  
 DB 404 GGAAAAAATGTAATCACTCACTACTGGAATTC 438

## RESULT 15

BP214869  
 LOCUS BP214869 Sugano cDNA library, corpus callosum Homo sapiens cDNA  
 DEFINITION clone CCR02053, mRNA sequence.  
 ACCESSION BP214869  
 VERSION BP214869.1 GI:52087770  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 579)  
 AUTHORS Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,  
 Mizushima-Sugano,J., Nakai,K. and Sugano,S.

TITLE Sequence comparison of human and mouse genes reveals a homologous  
 block structure in the promoter regions  
 JOURNAL Genome Res. 14 (9), 1711-1718 (2004)  
 COMMENT Contact: Yutaka Suzuki  
 Department of Virology  
 Institute of Medical Science, University of Tokyo  
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
 Email: ysuzuki@ims.u-tokyo.ac.jp.

## FEATURES

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 /clone\_lib="Sugano cDNA library, corpus callosum"

## ORIGIN

Query Match 42.0%; Score 374.2; DB 5; Length 579;  
 Best Local Similarity 99.2%; Pred. No. 1.1e-97;  
 Matches 376; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 86 CGCGCTCTCTTCTAGTCGGCGCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGAACTA 145  
 DB 183 CGCGCTCTCTTCTAGTCGGCGCATGACGACCGCGTCCACCTCGCAGGTGCGCCAGAACTA 242  
 QY 146 CCACAGAGACTCAGAGCGCGCATCAACCGCCAGATCAACCTGGAGCTTACGCTCTCTA 205  
 DB 243 CCACAGAGACTCAGAGCGCGCATCAACCGCCAGATCAACCTGGAGCTTACGCTCTCTA 302  
 QY 206 CGTTTACCTGTCCATGCTTACTACTTTTGACCGCGATGATGCTTGAAGAACTTTGC 265  
 DB 303 CGTTTACCTGTCCATGCTTACTACTTTTGACCGCGATGATGCTTGAAGAACTTTGC 362  
 QY 266 CAATATCTTTCTTCCAAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 325  
 DB 363 CAATATCTTTCTTCCAAATCTCATGAGGAGGGAACATGCTGAGAACTGATGAAGCT 422  
 QY 326 GCAGAACCAACGAGGTGGCCGAATCTTCTTCAGGATATCAAGAACCAAGACTGTGATGA 385  
 DB 423 GCAGAACCAACGAGGTGGCCGAATCTTCTTCAGGATATCAAGAACCAAGACTGTGATGA 482  
 QY 386 CTGGGAGAGCGGCTGAATGCAATGAGTGTGCATTACATTTGGAAAAAATGTGAATCA 445  
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 QY 446 GTCACCTAGTGAATTCCT 464  
 DB 543 GTCACCTAGTGAATTCCT 561

Search completed: April 1, 2005, 13:07:05  
 Job time : 2395 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 30, 2005, 19:33:36 ; Search time 176 Seconds  
(without alignment)  
480.074 Million cell updates/sec

Title: US-09-786-867C-5  
Perfect score: 893  
Sequence: 1 MTTASTSVQRNYHQDSEAA.....PRRRKRPHSIPTILIFRSP 165

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query	ID	Description
1	890	99.7	165	Q8TD27	Q8td27 homo sapien
2	615.5	68.9	232	Q6NS36	Q6ns36 homo sapien
3	610.5	68.4	182	Q6NS36	Q6ns36 homo sapien
4	605.5	67.8	183	Q6NZ44	Q6nz44 homo sapien
5	589.5	66.0	182	Q6NS36	Q6ns36 homo sapien
6	589.5	66.0	182	Q6NS36	Q6ns36 homo sapien
7	586.5	65.7	182	Q6NS36	Q6ns36 homo sapien
8	585	65.5	197	Q6P9V2	Q6p9v2 rattus norv
9	583.5	65.3	220	Q6H15	Q6h15 rattus norv
10	583.5	65.3	229	Q6AYV6	Q6ayv6 rattus norv
11	580.5	65.0	185	Q6NS36	Q6ns36 homo sapien
12	575.5	64.4	181	Q6NS36	Q6ns36 homo sapien
13	573.5	64.2	181	Q6NS36	Q6ns36 homo sapien
14	570.5	63.9	182	Q6NS36	Q6ns36 homo sapien
15	560.5	62.8	170	Q6NS36	Q6ns36 homo sapien
16	560.5	62.8	179	Q6NS36	Q6ns36 homo sapien
17	560.5	62.8	180	Q6NS36	Q6ns36 homo sapien
18	560.5	62.8	181	Q6NS36	Q6ns36 homo sapien
19	516.5	57.8	177	Q6NS36	Q6ns36 homo sapien
20	515.5	57.7	177	Q6NS36	Q6ns36 homo sapien
21	514.5	57.6	169	Q6NS36	Q6ns36 homo sapien
22	514.5	57.6	177	Q6NS36	Q6ns36 homo sapien
23	508.5	56.9	180	Q6NS36	Q6ns36 homo sapien
24	500.5	56.0	157	Q6NS36	Q6ns36 homo sapien
25	499.5	55.9	164	Q6NS36	Q6ns36 homo sapien
26	494	55.3	100	Q6NS36	Q6ns36 homo sapien
27	494	55.3	242	Q6NS36	Q6ns36 homo sapien
28	488.5	54.7	152	Q6NS36	Q6ns36 homo sapien
29	480	53.8	132	Q6NS36	Q6ns36 homo sapien
30	479	53.6	237	Q6NS36	Q6ns36 homo sapien
31	477	53.4	262	Q6NS36	Q6ns36 homo sapien

32	475	53.2	177	1	FRH_SALSA	P49946 salmo salar
33	469	52.5	177	2	Q8DDT0	Q8ddt0 brachydanio
34	460.5	51.6	175	2	Q801J6	Q801j6 scyllorhinu
35	458	51.3	177	2	Q66HX7	Q66hx7 brachydanio
36	457	51.2	92	2	Q862D5	Q862d5 bos taurus
37	456.5	51.1	127	2	Q862R4	Q862r4 bos taurus
38	453	50.7	176	2	Q98TT0	Q98tt0 oncorhynch
39	441	49.4	156	2	Q8EEB1	Q8eeb1 protopteris
40	440	49.3	177	2	Q801J5	Q801j5 petromyzon
41	439	49.2	173	1	FRIS_LYMST	P42577 lymaea sta
42	436	48.8	134	2	Q86QN8	Q86qn8 branchiosto
43	436	48.8	172	2	Q6WNW7	Q6wnw7 branchiosto
44	435.5	48.8	149	2	Q9GMG9	Q9gmg9 macaca mula
45	435.5	48.8	174	2	Q86LZ3	Q86lz3 branchiosto

ALIGNMENTS

RESULT 1

ID Q8TD27 PRELIMINARY; PRT; 165 AA.  
AC Q8TD27;  
DT 01-JUN-2002 (Tremblrel. 21, Created)  
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE Placenta immunoregulatory factor PLIF.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
SEQUENCE FROM N.A.  
RX MEDLINE=2193397; PubMed=11821435; DOI=10.1074/jbc.M200956200;  
RA Moroz C., Traub L., Maymon R., Zahalka M.A.;  
RT "PLIF, a novel human ferritin subunit from placenta with  
immunosuppressive activity";  
RL J. Biol. Chem. 277:12901-12905(2002).  
CC -1- SIMILARITY: Belongs to the ferritin family.  
CC -1- SIMILARITY: Contains 1 ferritin-like diiron domain.  
DR EMBL; AY033611; AAK55486.1; -;  
DR HSP; P02794; 2FHA.  
DR GO; GO:0005886; C:plasma membrane; NAS.  
DR GO; GO:0019900; F:kinase binding; NAS.  
DR GO; GO:0006955; P:immune response; IDA.  
DR GO; GO:0008285; P:negative regulation of cell proliferation; IDA.  
DR InterPro; IPR001519; Ferritin.  
DR InterPro; IPR009078; Ferritin/RR like.  
DR InterPro; IPR008331; Ferritin\_Dp.  
DR InterPro; IPR009040; Ferritin\_like.  
DR Pfam; PF00210; Ferritin; 1.  
DR ProDom; PD000971; Ferritin; 1.  
DR PROSITE; PS00540; FERRITIN\_1; 1.  
DR PROSITE; PS00905; FERRITIN\_LIKE; 1.  
KW Iron; Iron storage; Metal-Binding.  
SQ SEQUENCE 165 AA; 19490 MW; C4849C853FCABAB6 CRC64;

Query Match 99.7%; Score 890; DB 2; Length 165;  
Best Local Similarity 99.4%; Pred. No. 1.1e-71;  
Matches 164; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MTTASTSVQRNYHQDSEAAINRQINLELYASYVLSMSYFDRDDVAKNFKAYFLHQ	60
Db	1	MTTASTSVQRNYHQDSEAAINRQINLELYASYVLSMSYFDRDDVAKNFKAYFLHQ	60
Qy	61	HEERQHAELKMLQNGRIFLODIKKPCDDMESGLNAMECALHLEKNVNSLLEP	120
Db	61	HEERQHAELKMLQNGRIFLODIKKPCDDMESGLNAMECALHLEKNVNSLLEP	120
Qy	121	PISPSPCSWHYTTNRPOQHLLRPRRRKRPHSIPTILIFRSP	165
Db	121	PISPSPCSWHYTTNRPOQHLLRPRRRKRPHSIPTILIFRSP	165

RESULT 2  
Q6NS36 PRELIMINARY; PRT; 232 AA.  
AC Q6NS36;  
DT 05-JUL-2004 (TRENBLrel. 27, Created)  
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
DE FTH1 protein (Fragment).  
GN Name=FTH1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny K.D., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzyzanski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RA "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Strausberg R.;  
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron  
CC in a soluble, nontoxic, readily available form. The functional  
CC molecule, which is composed of 24 chains, is roughly spherical and  
CC contains a central cavity into which the polymeric ferric iron  
CC core is deposited (By similarity).  
CC -!- SIMILARITY: Belongs to the ferritin family.  
CC EMBL; BC070494; AAH70494.1; -.  
DR HSP; P02791; 1AEW.  
DR GO; GO:0005488; F:binding; IEA.  
DR GO; GO:0008199; F:ferric iron binding; IEA.  
DR GO; GO:0006879; P:iron ion homeostasis; IEA.  
DR GO; GO:0006826; P:iron ion transport; IEA.  
DR InterPro; IPR001519; Ferritin.  
DR InterPro; IPR009078; Ferritin/RR like.  
DR InterPro; IPR008331; Ferritin\_Dps.  
DR Pfam; PF00210; Ferritin; 1.  
DR ProDom; PD000971; Ferritin; 1.  
DR PROSITE; PS00540; FERRITIN\_1; 1.  
DR PROSITE; PS00204; FERRITIN\_2; 1.  
DR PROSITE; PS00905; FERRITIN\_LIKE; 1.  
KW Iron; iron storage; Metal-Binding.  
FT NON\_TER  
SQ SEQUENCE 232 AA; 26219 MW; 6C1756461G345A85 CRC64;

Query Match 68.9%; Score 615.5; DB 2; Length 232;  
Best Local Similarity 84.6%; Pred. No. 5.4e-47;  
Matches 121; Conservative 3; Mismatches 6; Indels 13; Gaps 2;

QY 1 MTTASTSQVRQNYHDSAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKIFLHQS 60  
DB |||||  
QY 50 MTTASTSQVRQNYHDSAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKIFLHQS 109  
DB |||||  
QY 61 HEERQHAELKMLQNGRGRIFLDIKKPCDDWESGLNAMECALHLEKNVNSLLEFPS 120  
DB |||||  
QY 110 HEERQHAELKMLQNGRGRIFLDIKKPCDDWESGLNAMECALHLEKNVNSLLEFPS 167  
DB |||||  
QY 121 PISPSPCSWHHYTTNRPPQPHL 143  
DB 168 -----HKLATDKNDP--HL 179  
PRT; 182 AA.  
RESULT 3  
FTH1 HUMAN  
ID FTH1 HUMAN STANDARD; PRT; 182 AA.  
AC P02794;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Ferritin heavy chain (Ferritin H subunit).  
GN Name=FTH1; Synonyms=FTH, FTHL6;  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86008223; PubMed=3840162;  
RA Boyd D., Vecoli C., Belcher D.M., Jain S.K., Drysdale J.W.;  
RA "Structural and functional relationships of human ferritin H and L  
RT chains deduced from cDNA clones.";  
RL J. Biol. Chem. 260:11755-11761 (1985).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86120367; PubMed=3003694;  
RA Costanzo F., Colombo M., Staempfli S., Santoro C., Marone M.,  
RA Frank R., Delius H., Cortese R.;  
RA "Structure of gene and pseudogenes of human apoferritin H.";  
RL Nucleic Acids Res. 14:721-736 (1986).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver parenchymal cells;  
RX MEDLINE=84158533; PubMed=632167;  
RA Costanzo F., Santoro C., Colantuoni V., Bensi G., Raugi G.,  
RA Romano V., Cortese R.;  
RA "Cloning and sequencing of a full length cDNA coding for a human  
RT apoferritin H chain: evidence for a multigene family.";  
RL EMBO J. 3:23-27 (1984).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87064341; PubMed=3023856;  
RA Chou C.-C., Gatti R.A., Fuller M.L., Concannon P., Wong A., Chada S.,  
RA Davis R.C., Salser W.A.;  
RA "Structure and expression of ferritin genes in a human promyelocytic  
RT cell line that differentiates in vitro.";  
RL Mol. Cell. Biol. 6:566-573 (1986).  
RN [5]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87016920; PubMed=3020541;  
RA Hentze M.W., Klem S., Papadopoulos P., O'Brien S., Modi W.,  
RA Drysdale J.W., Leonard W.J., Harford J.B., Klausner R.D.;  
RA "Cloning, characterization, expression, and chromosomal localization  
RT of a human ferritin heavy-chain gene.";  
RL Proc. Natl. Acad. Sci. U.S.A. 83:7226-7230 (1986).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=93246257; PubMed=7916709; DOI=10.1016/0378-1119(93)90380-L;  
RA Dhar M., Chauthaiwale V.M., Joshi J.G.;  
RT "Sequence of a cDNA encoding the ferritin H-chain from an 11-week-old  
human fetal brain.";  
RL Gene 126:275-278 (1993).

[7]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Chauthaiwalé V.M., Dhar M., McLachlan D.R., Joshi J.G.;  
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
 [8]  
 RP SEQUENCE FROM N.A.  
 RA Franco A.V., Gray C.P., Myers K., Hersey P.;  
 RT "Detection of ferritin heavy chain by SEREX: a multifunctional  
 molecule in malignant tumour cells."  
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
 [9]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Colon adenocarcinoma;  
 RA Shichijo S., Itoh K.;  
 RT "Identification of immuno-peptidomimics that recognized by tumor-reactive  
 CTL generated from TIL of colon cancer patients."  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 [10]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain, Cervix, Colon, Lung, Ovary, and Prostate;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshikiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [11]  
 RP SEQUENCE OF 127-182 FROM N.A.  
 RX MEDLINE=84272711; PubMed=6589621;  
 RA Boyd D., Jain S.K., Crampton J., Barrett K.J., Drysdale J.;  
 RT "Isolation and characterization of a cDNA clone for human ferritin  
 heavy chain."  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:4751-4755(1984).  
 [12]  
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).  
 RX MEDLINE=91125486; PubMed=1992356; DOI=10.1038/349541a0;  
 RA Lawson D.M., Artymniuk P.J., Yewdall S.J., Smith J.M.A.;  
 RA Livingstone J.C., Treffry A., Luzzago A., Levi S., Arosio P.,  
 RA Cesarini G., Thomas C.D., Shaw W.W., Harrison P.M.;  
 RT "Solving the structure of human H ferritin by genetically engineering  
 intermolecular crystal contacts."  
 RL Nature 349:541-544(1991).  
 [13]  
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS)  
 RX MEDLINE=97303050; PubMed=9159481; DOI=10.1006/jmbi.1997.0970;  
 RA Hempstead P.D., Yewdall S.J., Fernie A.R., Lawson D.M., Artymniuk P.J.,  
 RA Rice D.W., Ford G.C., Harrison P.M.;  
 RT "Comparison of the three-dimensional structures of recombinant human H  
 and horse L ferritins at high resolution."  
 RL J. Mol. Biol. 268:424-448(1997).  
 CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron  
 in a soluble, nontoxic, readily available form. The functional  
 molecule, which is composed of 24 chains, is roughly spherical and  
 contains a central cavity into which the polymeric ferric iron  
 core is deposited.  
 CC -!- MISCELLANEOUS: There are two types of ferritin subunits: L (light)  
 chain and H (heavy) chain. The major chain can be light or heavy,  
 depending on the species and tissue type.  
 CC -!- MISCELLANEOUS: In human liver the heavy chain is the major chain.  
 CC -!- SIMILARITY: Belongs to the ferritin family.  
 CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.  
 CC -!- CAUTION: Ref.3 sequence differs from that shown due to a  
 frameshift in position 175.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; M11146; AAA52437.1; -;  
 DR EMBL; X03487; CAA27205.1; -;  
 DR EMBL; X03488; CAA27205.1; JOINED.  
 DR EMBL; X00318; CAA25086.1; ALT\_FRAME.  
 DR EMBL; M14212; AAA52438.1; -;  
 DR EMBL; M14211; AAA52438.1; JOINED.  
 DR EMBL; M12937; AAA35830.1; -;  
 DR EMBL; M15383; AAA52479.1; -;  
 DR EMBL; L20941; AAA35833.1; -;  
 DR EMBL; AF088851; AAF89523.1; -;  
 DR EMBL; AB082402; BAB93489.1; -;  
 DR EMBL; BC000857; AAH00857.1; -;  
 DR EMBL; BC001399; AAH01399.1; -;  
 DR EMBL; BC011359; AAH11359.1; -;  
 DR EMBL; BC013724; AAH13724.1; -;  
 DR EMBL; BC015156; AAH15156.1; -;  
 DR EMBL; BC016009; AAH16009.1; -;  
 DR EMBL; BC016857; AAH16857.1; -;  
 DR EMBL; BC066961; AAH66961.1; -;  
 DR EMBL; M97164; AAA5832.1; -;  
 DR PIR; A23517; FRHUH.  
 DR PDB; 1FHA; X-ray; @=1-182.  
 DR PDB; 2FHA; X-ray; @=1-182.  
 DR Genew; HGNC:3976; FTH1.  
 DR H-InvDB; HIX0009704; -;  
 DR MIM; 134770; -;  
 DR GO; GO:0008043; C:ferritin complex; TAS.  
 DR GO; GO:0005886; C:plasma membrane; ISS.  
 DR GO; GO:0005506; F:iron ion binding; TAS.  
 DR GO; GO:0019900; F:kinase binding; ISS.  
 DR GO; GO:0008283; P:cell proliferation; TAS.  
 DR GO; GO:0006955; P:immune response; ISS.  
 DR GO; GO:0006880; P:intracellular iron ion storage; TAS.  
 DR GO; GO:0008285; P:negative regulation of cell proliferation; ISS.  
 DR InterPro; IPR001519; Ferritin.  
 DR InterPro; IPR009078; Ferritin/RR\_like.  
 DR InterPro; IPR008331; Ferritin\_Dps.  
 DR InterPro; IPR009040; Ferritin\_Like.  
 DR Pfam; PF00210; Ferritin; 1.  
 DR ProDom; PD000971; Ferritin; 1.  
 DR PROSITE; PS00540; FERRITIN\_1; 1.  
 DR PROSITE; PS00204; FERRITIN\_2; 1.  
 DR PROSITE; PS09055; FERRITIN\_Like; 1.  
 KW 3D-structure; Iron; Iron storage; Metal-binding.  
 FT INIT MET 0  
 FT DOMAIN 10 159 Ferritin-like diiron.  
 FT METAL 27 27 Iron.  
 FT METAL 58 58 Iron.  
 FT METAL 61 61 Iron.  
 FT METAL 62 62 Iron.  
 FT METAL 64 64 Iron.  
 FT METAL 65 65 Iron.  
 FT METAL 107 107 Iron.  
 FT METAL 141 141 Iron.  
 Query Match 68.4%; Score 610.5; DB 1; Length 182;  
 Best Local Similarity 84.5%; Pred. No. 1.1e-46;  
 Matches 120; Conservative 3; Mismatches 6; Indels 13; Gaps 2;

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QY 2 TTASTSQVRQNYHQDSEAINRQINLELYASYVYLSMSYFFDRDDVAKNFYFLHOSH 61
|||||
Db 1 TTASTSQVRQNYHQDSEAINRQINLELYASYVYLSMSYFFDRDDVAKNFYFLHOSH 60
|||||
QY 62 EERQHAELKMLQNGRGRIFLODIKKPDCDDWESGLNAMECALHLEKNVNSLLEFPSP 121
|||||
Db 61 EERHAELKMLQNGRGRIFLODIKKPDCDDWESGLNAMECALHLEKNVNSLLEL--- 117
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QY 122 ISPSPSCWHYTTNRPOQHHL 143
|||||
Db 118 -----HKLATDKNDP--HL 129
|||||

RESULT 4
Q6NZ44 PRELIMINARY; PRT; 183 AA.
ID Q6NZ44
AC Q6NZ44;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron
CC in a soluble, nontoxic, readily available form. The functional
CC molecule, which is composed of 24 chains, is roughly spherical and
CC contains a central cavity into which the polymeric ferric iron
CC core is deposited (by similarity).
CC
CC -!- SIMILARITY: Belongs to the ferritin family.
CC
CC EMBL; BC06341; AAH66341.1; -.
DR HSSP; P02791; 1AEW.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR001519; Ferritin.
DR InterPro; IPR009078; Ferritin/RR like.
DR InterPro; IPR008331; Ferritin_Dps.
DR InterPro; IPR009040; Ferritin_like.
DR Pfam; PF00210; Ferritin; 1.

QY 1 MTTASTSQVRQNYHQDSEAINRQINLELYASYVYLSMSYFFDRDDVAKNFYFLHQS 60
|||||
Db 1 MTTASTSQVRQNYHQDSEAINRQINLELYASYVYLSMSYFFDRDDVAKNFYFLHQS 60
|||||
QY 61 HEERQHAELKMLQNGRGRIFLODIKKPDCDDWESGLNAMECALHLEKNVNSLLEPPS 120
|||||
Db 61 HEERHAELKMLQNGRGRIFLODIKKPDCDDWESGLNAMECALHLEKNVNSLLEL-- 118
|||||
QY 121 PISPSPSCWHYTTNRPOQHHL 143
|||||
Db 119 -----HKLATDKNDP--HL 130
|||||

RESULT 5
FRIH TRIVU STANDARD; PRT; 182 AA.
ID FRIH TRIVU
AC Q9XT73;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ferritin heavy chain (Ferritin H subunit).
GN Name=PTH; Synonyms=FRIH;
OS Trichosurus vulpecula (Brush-tailed possum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Diprotodontia; Phalangeridae; Trichosurus.
OX NCBI_TaxID=9337;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lactating mammary gland;
RX MEDLINE=92227120; PubMed=10209259; DOI=10.1016/S0167-4781(99)00042-1;
RA Denner J., Scastuk S.J., Adamski F.M., Grigor M.R.;
RT "Cloning and expression of the transferrin and ferritin genes in a
RL marsupial, the brushtail possum (Trichosurus vulpecula).";
RL Biochim. Biophys. Acta 1445:65-74(1999).
CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron
CC in a soluble, nontoxic, readily available form. The functional
CC molecule, which is composed of 24 chains, is roughly spherical and
CC contains a central cavity into which the polymeric ferric iron
CC core is deposited (by similarity).
CC
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC
CC -!- SIMILARITY: Belongs to the ferritin family.
CC
CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sb-sib.ch).
CC
CC EMBL; AF092509; AAD38330.1; -.
DR HSSP; P02794; 2FHA.
DR GO; GO:0005886; C:plasma membrane; ISS.
DR GO; GO:0019900; F:kinase binding; ISS.
DR GO; GO:0006955; P:immune response; ISS.
DR GO; GO:0008285; P:negative regulation of cell proliferation; ISS.
DR InterPro; IPR001519; Ferritin.
DR InterPro; IPR009078; Ferritin/RR like.
DR InterPro; IPR008331; Ferritin_Dps.
DR InterPro; IPR009040; Ferritin_like.
DR Pfam; PF00210; Ferritin; 1.
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DR ProDom; PD000971; Ferritin; 1.
DR PROSITE; PS00540; FERRITIN_1; 1.
DR PROSITE; PS00204; FERRITIN_2; 1.
DR PROSITE; PS09095; FERRITIN LIKE; 1.
KW Hypothetical protein; Iron; Iron storage; Metal-binding.
SQ SEQUENCE 183 AA; 21441 MW; 4512B8078A2320B2 CRC64;

Query Match 67.8%; Score 605.5; DB 2; Length 183;
Best Local Similarity 83.2%; Pred. No. 3.2e-46;
Matches 119; Conservative 4; Mismatches 7; Indels 13; Gaps 2;

QY 1 MTTASTSQVRQNYHQDSEAINRQINLELYASYVYLSMSYFFDRDDVAKNFYFLHQS 60
|||||
Db 1 MTTASTSQVRQNYHQDSEAINRQINLELYASYVYLSMSYFFDRDDVAKNFYFLHQS 60
|||||
QY 61 HEERQHAELKMLQNGRGRIFLODIKKPDCDDWESGLNAMECALHLEKNVNSLLEPPS 120
|||||
Db 61 HEERHAELKMLQNGRGRIFLODIKKPDCDDWESGLNAMECALHLEKNVNSLLEL-- 118
|||||
QY 121 PISPSPSCWHYTTNRPOQHHL 143
|||||
Db 119 -----HKLATDKNDP--HL 130
|||||

RESULT 5
FRIH TRIVU STANDARD; PRT; 182 AA.
ID FRIH TRIVU
AC Q9XT73;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ferritin heavy chain (Ferritin H subunit).
GN Name=PTH; Synonyms=FRIH;
OS Trichosurus vulpecula (Brush-tailed possum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Diprotodontia; Phalangeridae; Trichosurus.
OX NCBI_TaxID=9337;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lactating mammary gland;
RX MEDLINE=92227120; PubMed=10209259; DOI=10.1016/S0167-4781(99)00042-1;
RA Denner J., Scastuk S.J., Adamski F.M., Grigor M.R.;
RT "Cloning and expression of the transferrin and ferritin genes in a
RL marsupial, the brushtail possum (Trichosurus vulpecula).";
RL Biochim. Biophys. Acta 1445:65-74(1999).
CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron
CC in a soluble, nontoxic, readily available form. The functional
CC molecule, which is composed of 24 chains, is roughly spherical and
CC contains a central cavity into which the polymeric ferric iron
CC core is deposited (by similarity).
CC
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC
CC -!- SIMILARITY: Belongs to the ferritin family.
CC
CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sb-sib.ch).
CC
CC EMBL; AF092509; AAD38330.1; -.
DR HSSP; P02794; 2FHA.
DR GO; GO:0005886; C:plasma membrane; ISS.
DR GO; GO:0019900; F:kinase binding; ISS.
DR GO; GO:0006955; P:immune response; ISS.
DR GO; GO:0008285; P:negative regulation of cell proliferation; ISS.
DR InterPro; IPR001519; Ferritin.
DR InterPro; IPR009078; Ferritin/RR like.
DR InterPro; IPR008331; Ferritin_Dps.
DR InterPro; IPR009040; Ferritin_like.
DR Pfam; PF00210; Ferritin; 1.
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DR ProDom; PD000971; Ferritin; 1.
DR PROSITE; PS00540; FERRITIN_1; 1.
DR PROSITE; PS00204; FERRITIN_2; 1.
DR PROSITE; PS00905; FERRITIN_LIKE; 1.
KW Iron; Iron storage; Metal-Binding.
FT INIT MET 0 0 By similarity.
FT DOMAIN 10 159 Ferritin-like diiron.
FT METAL 27 27 Iron (By similarity).
FT METAL 61 61 Iron (By similarity).
FT METAL 62 62 Iron (By similarity).
FT METAL 65 65 Iron (By similarity).
FT METAL 107 107 Iron (By similarity).
FT METAL 141 141 Iron (By similarity).
SQ SEQUENCE 182 AA; 21163 MW; 22C85B4AC8C852P CRC64;

Query Match 66.0%; Score 589.5; DB 1; Length 182;
Best Local Similarity 82.4%; Pred. No. 8.5e-45;
Matches 117; Conservative 4; Mismatches 8; Indels 13; Gaps 2;

QY 2 TTASTSQVRQNYHQDSEAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYFLHOSH 61
Db 1 TTSSPSQVRQNYHQDSEAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYFLHOSH 60
QY 62 EERQHAELKMLQNGRGRIFLDQIKKPCDDWESGLNAMECALHLEKNVNSQLLEPSP 121
Db 61 EEREHAELKMLQNGRGRIFLDQIKKPCDDWESGLNAMECALHLEKNVNSQLLEPSP 117
QY 122 ISPSPCSWHHYTTNRPOQHHL 143
Db 118 -----HKLATDKNDP--HL 129

RESULT 6
Q95MP7
ID Q95MP7 PRELIMINARY; PRT; 183 AA.
AC Q95MP7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Ferritin.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Jeoung D., Jung D., Kim H.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron
CC in a soluble, nontoxic, readily available form. The functional
CC molecule, which is composed of 24 chains, is roughly spherical and
CC contains a central cavity into which the polymeric ferric iron
CC core is deposited (By similarity).
CC -!- SIMILARITY: Belongs to the ferritin family.
CC EMBL; AF285177; AAK82992.1; -.
DR HSSP; P02794; 2FHA.
DR GO; GO:0005886; C:plasma membrane; ISS.
DR GO; GO:0019900; P:kinase binding; ISS.
DR GO; GO:0006955; P:immune response; ISS.
DR GO; GO:0008285; P:negative regulation of cell proliferation; ISS.
DR InterPro; IPR001519; Ferritin.
DR InterPro; IPR009078; Ferritin/RR-like.
DR InterPro; IPR008331; Ferritin_Dps.
DR InterPro; IPR009040; Ferritin_Like.
DR Pfam; PF00210; Ferritin; 1.
DR ProDom; PD000971; Ferritin; 1.
DR PROSITE; PS00540; FERRITIN_1; 1.
DR PROSITE; PS00204; FERRITIN_2; 1.
DR PROSITE; PS00905; FERRITIN_LIKE; 1.
KW Iron; Iron storage; Metal-Binding.
SQ SEQUENCE 183 AA; 21308 MW; 9D22750A1AC4BE72 CRC64;

Query Match 66.0%; Score 589.5; DB 2; Length 183;
Best Local Similarity 81.8%; Pred. No. 1.6e-44;
Matches 116; Conservative 6; Mismatches 8; Indels 13; Gaps 2;

QY 1 MTTASTSQVRQNYHQDSEAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYFLHQS 60
Db 1 MTTASPSQVRQNYHQDSEAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYFLHQS 60
QY 61 HEERQHAELKMLQNGRGRIFLDQIKKPCDDWESGLNAMECALHLEKNVNSQLLEPSP 120
Db 61 HEEREHAELKMLQNGRGRIFLDQIKKPCDDWESGLNAMECALHLEKSNQSLLEPSP 118
QY 121 PISPSPCSWHHYTTNRPOQHHL 143
Db 119 -----HKLATDKNDP--HL 130

RESULT 7
Q920K4
ID Q920K4 PRELIMINARY; PRT; 182 AA.
AC Q920K4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Ferritin heavy chain.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Hartley; TISSUE=Spleen;
RA Takagi R., Ohtani M., Watanabe N., Kobayashi Y.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron
CC in a soluble, nontoxic, readily available form. The functional
CC molecule, which is composed of 24 chains, is roughly spherical and
CC contains a central cavity into which the polymeric ferric iron
CC core is deposited (By similarity).
CC -!- SIMILARITY: Belongs to the ferritin family.
CC EMBL; AB073371; BAB70615.1; -.
DR HSSP; P02794; 2FHA.
DR GO; GO:0005886; C:plasma membrane; ISS.
DR GO; GO:0019900; P:kinase binding; ISS.
DR GO; GO:0006955; P:immune response; ISS.
DR GO; GO:0008285; P:negative regulation of cell proliferation; ISS.
DR Pfam; PF00210; Ferritin; 1.
DR ProDom; PD000971; Ferritin; 1.
DR PROSITE; PS00540; FERRITIN_1; 1.
DR PROSITE; PS00204; FERRITIN_2; 1.
DR PROSITE; PS00905; FERRITIN_LIKE; 1.
KW Iron; Iron storage; Metal-Binding.
SQ SEQUENCE 182 AA; 21163 MW; E5E12825DE10BE66 CRC64;

Query Match 65.7%; Score 586.5; DB 2; Length 182;
Best Local Similarity 81.1%; Pred. No. 1.6e-44;
Matches 116; Conservative 6; Mismatches 8; Indels 13; Gaps 2;

QY 1 MTTASTSQVRQNYHQDSEAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYFLHQS 60
Db 1 MTTASPSQVRQNYHQDSEAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYFLHQS 60
QY 61 HEERQHAELKMLQNGRGRIFLDQIKKPCDDWESGLNAMECALHLEKNVNSQLLEPSP 120
Db 61 HEEREHAELKMLQNGRGRIFLDQIKKPCDDWESGLNAMECALHLEKSNQSLLEPSP 118
QY 121 PISPSPCSWHHYTTNRPOQHHL 143
Db 119 -----HKLATDKNDP--HL 130

RESULT 8

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121 PISPSPCWHHYTTNRPQPQ-----HLL 144



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Db 157 -----HKLATDKNDP--HL 168

RESULT 10
Q6AYV6 PRELIMINARY; PRT; 229 AA.
ID Q6AYV6
AC Q6AYV6
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE Fth1 protein (Fragment).
GN Name=Fth1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
EX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Skalsoda J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Grimwood U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Director MCC Project;
RA Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron
CC in a soluble, nontoxic, readily available form. The functional
CC molecule, which is composed of 24 chains, is roughly spherical and
CC contains a central cavity into which the polymeric ferric iron
CC core is deposited (By similarity).
CC -!- SIMILARITY: Belongs to the ferritin family.
CC EMBL; BC078892; AAH78892.1; -.
CC GO; GO:0005488; F:binding; IEA.
CC GO; GO:0008199; F:ferric iron binding; IEA.
CC GO; GO:0006879; P:iron ion homeostasis; IEA.
CC GO; GO:0006826; P:iron ion transport; IEA.
CC InterPro; IPR001519; Ferritin.
CC InterPro; IPR009078; Ferritin/RR like.
CC InterPro; IPR008331; Ferritin_Dps.
CC Pfam; PF00210; Ferritin; 1.
CC ProDom; PD000971; Ferritin; 1.
CC ProDom; PD000371; Ferritin; 1.
CC PROSITE; PS00540; FERRITIN_1; 1.
CC PROSITE; PS00204; FERRITIN_2; 1.
CC PROSITE; PS0305; FERRITIN_LIKE; 1.
KW Iron; Iron storage; Metal-Binding.
FT NON_TER
SQ SEQUENCE 229 AA; 26026 MW; BD826EA2B682D74B CRC64;

Query Match 65.3%; Score 583.5; DB 2; Length 229;
Best Local Similarity 81.8%; Pred. No. 3.8e-44;
Matches 117; Conservative 4; Mismatches 9; Indels 13; Gaps 2;

QY 1 MTTASTSVQVRYNHODSEAAINRQINLELYASYVYLSMSYFDRDDVALKNPKAFYFLHQS 60
DB 48 MTTASPSQVRYNHODSEAAINRQINLELYASYVYLSMSYFDRDDVALKNPKAFYFLHQS 107
QY 61 HEERQHAELKMLQNGRGRIPLQDIKKPDCDDWESGLNAMECALHLEKNVQNSLLEPFS 120
DB 108 HEERHAELKMLQNGRGRIPLQDIKKPDCDDWESGLNAMECALHLEKNVQNSLLEPFS 165
QY 121 PISPSPCSWHHYTTNRPOQHHL 143
DB 166 -----HKLATDKNDP--HL 177

RESULT 11
FRIH CRIGR STANDARD; PRT; 185 AA.
ID FRIH CRIGR
AC P29389;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DE Ferritin heavy chain (Ferritin H subunit).
GN Name=FTH;
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
EX MEDLINE=92375120; PubMed=1380656; DOI=10.1016/0921-8777(92)90069-F;
RA Zhu W., Keng P., Chou W.G.;
RT "Differential gene expression in wild-type and X-ray-sensitive mutants
RT of Chinese hamster ovary cell lines."
RL Mutat. Res. 274:237-245 (1992).
CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron
CC in a soluble, nontoxic, readily available form. The functional
CC molecule, which is composed of 24 chains, is roughly spherical and
CC contains a central cavity into which the polymeric ferric iron
CC core is deposited.
CC -!- MISCELLANEOUS: There are two types of ferritin subunits: L (light)
CC chain and H (heavy) chain. The major chain can be light or heavy,
CC depending on the species and tissue type.
CC -!- SIMILARITY: Belongs to the ferritin family.
CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.
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CC or send an email to license@isb-sib.ch).
CC EMBL; M99692; AAB46388.1; -.
CC HSSP; P02794; 2PHA.
CC GO; GO:0005886; C:plasma membrane; ISS.
CC GO; GO:0019900; F:kinase binding; ISS.
CC GO; GO:0006955; P:immune response; ISS.
CC GO; GO:0008285; P:negative regulation of cell proliferation; ISS.
CC InterPro; IPR001519; Ferritin.
CC InterPro; IPR009078; Ferritin/RR like.
CC InterPro; IPR008331; Ferritin_Dps.
CC Pfam; PF00210; Ferritin; 1.
CC ProDom; PD000971; Ferritin; 1.
CC PROSITE; PS00540; FERRITIN_1; 1.
CC PROSITE; PS00204; FERRITIN_2; 1.
CC PROSITE; PS0305; FERRITIN_LIKE; 1.
KW Iron; Iron storage; Metal-Binding.
FT INIT_MET 0 0 By similarity.
FT DOMAIN 15 164 Ferritin-like diiron.
FT METAL 32 32 Iron (By similarity).
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FT METAL 63 Iron (By similarity).
FT METAL 66 Iron (By similarity).
FT METAL 67 Iron (By similarity).
FT METAL 69 Iron (By similarity).
FT METAL 70 Iron (By similarity).
FT METAL 112 Iron (By similarity).
FT METAL 146 Iron (By similarity).
SQ SEQUENCE 185 AA; 21355 MW; E665373DF43C82C4 CRC64;

Query Match 65.0%; Score 580.5; DB 1; Length 185;
Best Local Similarity 81.1%; Pred.No. 5.5e-44;
Matches 116; Conservative 5; Mismatches 9; Indels 13; Gaps 2;

QY 1 MTTASTSVQRVYHODSEAINRQINLELYASYVYLSMSYFFDRDDVALKNFYFLHQS 60
DB 5 LTTASPSQVRVYHODSEAINRQINLELYASYVYLSMSYFFDRDDVALKNFYFLHQS 64

QY 61 HEERQHAELKMLQNGRGRIFLODIKKPDCDDWESGLNAMECALHLEKYNQSLLEPPS 120
DB 65 HEERHAELKMLQNGRGRIFLODIKKPDRDDWESGLNAMECALHLEKSVNQSLEL-- 122

QY 121 PISPSPCWYHTNRPOQHLL 143
DB 123 -----HKLATDKNDP--HL 134

RESULT 12
PRIH MOUSE
ID PRIH_MOUSE STANDARD; PRT; 181 AA.
AC P09528;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ferritin heavy chain (Ferritin H subunit).
GN Name=Fch;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/c;
RX MEDLINE=90016900; PubMed=2798146;
RA Yachau A., Renaudie F., Grandchamp B., Beaumont C.;
RT "Nucleotide sequence of the mouse ferritin H chain gene.";
RL Nucleic Acids Res. 17:8005-8005(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=Macrophage;
RX MEDLINE=89057487; PubMed=3194211;
RA Miyazaki Y., Setoguchi M., Higuchi Y., Yoshida S., Akizuki S.,
RA Yamamoto S.;
RT "Nucleotide sequence of cDNA encoding the heavy subunit of mouse
RT macrophage ferritin.";
RL Nucleic Acids Res. 16:10373-10373(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=89315064; PubMed=3410854;
RA Torti S.V., Kwak E.L., Miller S.C., Miller L.L., Ringold G.M.,
RA Myambo K.B., Young A.P., Torti F.M.;
RT "The molecular cloning and characterization of murine ferritin heavy
RT chain, a tumor necrosis factor-inducible gene.";
RL J. Biol. Chem. 263:12638-12644(1988).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=91078648; PubMed=2258056; DOI=10.1016/0378-1119(90)90396-9;
RA Kwak E.L., Torti S.V., Torti F.M.;
RT "Murine ferritin heavy chain: isolation and characterization of a
RT functional gene.";
RL Gene 94:255-261(1990).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=89214195; PubMed=2708374;
```

```
RA Beaumont C., Dugast I., Renaudie F., Souroujon M., Grandchamp B.;
RT "Transcriptional regulation of ferritin H and L subunits in adult
RT erythroid and liver cells from the mouse. Unambiguous identification
RT of mouse ferritin subunits and in vitro formation of the ferritin
RT shells.";
RL J. Biol. Chem. 264:7498-7504(1989).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamakawa I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kaplan A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla B., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Meglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Negashima T., Nunata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP SEQUENCE FROM N.A.
RX MEDLINE=91078648; PubMed=2258056; DOI=10.1016/0378-1119(90)90396-9;
RA Kwak E.L., Torti S.V., Torti F.M.;
RT "Murine ferritin heavy chain: isolation and characterization of a
RT functional gene.";
RL Gene 94:255-261(1990).
RN [9]
RP SEQUENCE FROM N.A.
RX MEDLINE=89214195; PubMed=2708374;
```

-!- FUNCTION: Ferritin is an intracellular molecule that stores iron in a soluble, nontoxic, readily available form. The functional molecule, which is composed of 24 chains, is roughly spherical and contains a central cavity into which the polymeric ferric iron core is deposited.

-!- MISCELLANEOUS: There are two types of ferritin subunits: L (light) chain and H (heavy) chain. The major chain can be light or heavy, depending on the species and tissue type.

-!- SIMILARITY: Belongs to the ferritin family.

-!- SIMILARITY: Contains 1 ferritin-like diiron domain.



```
FT INIT MET 0 0 Ferritin-like diiron.
FT DOMAIN 10 159 Iron (By similarity).
FT METAL 27 27 Iron (By similarity).
FT METAL 61 61 Iron (By similarity).
FT METAL 62 62 Iron (By similarity).
FT METAL 65 65 Iron (By similarity).
FT METAL 107 107 Iron (By similarity).
FT METAL 141 141 Iron (By similarity).
FT METAL 181 181 R -> E (in Ref. 2).
FT CONFLICT 181 181 S -> E (in Ref. 4).
SQ SEQUENCE 181 AA; 20995 MW; 0A5AD533E1706C1 CRC64;

Query Match 64.2%; Score 573.5; DB 1; Length 181;
Best Local Similarity 81.0%; Pred. No. 2.3e-43;
Matches 115; Conservative 4; Mismatches 10; Indels 13; Gaps 2;

QY 2 TTASTSQVRNYHQDSEAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYLHQSH 61
DB 1 TTASPSQVRNYHQDSEAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYLHQSH 60
QY 62 EEROHAELKMLQNGRGRIFLQDIKKPDCDDWESGLNAMECALHLEKNVNSQLLEFPSP 121
DB 61 EEREHAELKMLQNGRGRIFLQDIKKPDCDDWESGLNAMECALHLEKNVNSQLLEL--- 117
QY 122 ISPSPCSWHYTNRPOQHLL 143
DB 118 -----HKLATDKNDP--HL 129

RESULT 14
QBMIP0 PRELIMINARY; PRT; 182 AA.
AC QBMIP0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ferritin heavy chain.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Takafuji V.A., Sharova L.V., Crisman M.V., Howard R.D.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron
in a soluble, nontoxic, readily available form. The functional
molecule, which is composed of 24 chains, is roughly spherical and
contains a central cavity into which the polymeric ferric iron
core is deposited (By similarity).
CC -!- SIMILARITY: Belongs to the ferritin family.
CC EMBL; AY112742; XAM51631.1; -.
DR HSP; P02794; 2FHA.
DR GO; GO:0005886; C:plasma membrane; ISS.
DR GO; GO:0019900; F:kinase binding; ISS.
DR GO; GO:0006955; P:immune response; ISS.
DR GO; GO:0008285; P:negative regulation of cell proliferation; ISS.
DR InterPro; IPR001519; Ferritin/RR like.
DR InterPro; IPR009078; Ferritin/RR like.
DR InterPro; IPR008331; Ferritin_Dps.
DR InterPro; IPR009040; Ferritin_like.
DR Pfam; PF00210; Ferritin; 1.
DR ProDom; PD000971; Ferritin; 1.
DR PROSITE; PS00540; FERRITIN_1; 1.
DR PROSITE; PS00204; FERRITIN_2; 1.
DR PROSITE; PS00905; FERRITIN-LIKE; 1.
KW Iron; Iron storage; Metal-Binding.
SQ SEQUENCE 182 AA; 21269 MW; 2282186D630F1A0D CRC64;

Query Match 63.9%; Score 570.5; DB 2; Length 182;
Best Local Similarity 79.0%; Pred. No. 4.2e-43;
Matches 113; Conservative 7; Mismatches 10; Indels 13; Gaps 2;
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QY 1 MTTASTSQVRNYHQDSEAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYLHQSH 60
DB 1 MTTAFPSQVRNYHQDSEAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYLHQSH 60
QY 61 HEEROHAELKMLQNGRGRIFLQDIKKPDCDDWESGLNAMECALHLEKNVNSQLLEFPSP 120
DB 61 HEEREHAELKMLQNGRGRIFLQDIKKPDCDDWENGLKAMECALHLEKNVNSLLEL-- 118
QY 121 PISPSPCSWHYTNRPOQHLL 143
DB 119 -----HKLATDKNDP--HL 130

RESULT 15
FRIH SHEEP STANDARD; PRT; 170 AA.
AC P18685;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ferritin heavy chain (Ferritin H subunit).
CN Name=ETH;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97073147; PubMed=8915895;
RX DOI=10.1002/(SICI)1097-4547(19961015)46:2<187::AID-JNR6>3.3.CO;2-J;
RA Sanyal B., Polak P.E., Szuchet S.;
RT "Differential expression of the heavy-chain ferritin gene in non-
adhered and adhered oligodendrocytes.";
RL J. Neurosci. Res. 46:187-197(1996).
[2]
SEQUENCE OF 71-101.
MEDLINE=89286137; PubMed=2472118;
MC Kenzie R.A., Yablonski M.J., Gillespie G.Y., Theil E.C.;
RT "Crosslinks between intramolecular pairs of ferritin subunits: effects
on both H and L subunits and on immunoreactivity of sheep spleen
ferritin.";
RL Arch. Biochem. Biophys. 272:88-96(1989).
CC -!- FUNCTION: Ferritin is an intracellular molecule that stores iron
in a soluble, nontoxic, readily available form. The functional
molecule, which is composed of 24 chains, is roughly spherical and
contains a central cavity into which the polymeric ferric iron
core is deposited.
CC -!- MISCELLANEOUS: There are two types of ferritin subunits: L (light)
chain and H (heavy) chain. The major chain can be light or heavy,
depending on the species and tissue type.
CC -!- SIMILARITY: Belongs to the ferritin family.
CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.
---
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---
EMBL; U54800; AAB19186.1; -.
DR HSP; P02794; 2FHA.
DR GO; GO:0005886; C:plasma membrane; ISS.
DR GO; GO:0019900; F:kinase binding; ISS.
DR GO; GO:0006955; P:immune response; ISS.
DR GO; GO:0008285; P:negative regulation of cell proliferation; ISS.
DR InterPro; IPR001519; Ferritin.
DR InterPro; IPR009078; Ferritin/RR like.
DR InterPro; IPR008331; Ferritin_Dps.
DR InterPro; IPR009040; Ferritin_like.
DR Pfam; PF00210; Ferritin; 1.
DR ProDom; PD000971; Ferritin; 1.
DR PROSITE; PS00540; FERRITIN_1; 1.
DR PROSITE; PS00204; FERRITIN_2; 1.
DR PROSITE; PS00905; FERRITIN-LIKE; 1.
KW Iron; Iron storage; Metal-Binding.
SQ SEQUENCE 182 AA; 21269 MW; 2282186D630F1A0D CRC64;
```

```
DR InterPro; IPR009040; Ferritin_like.
DR Pfam; PF00210; Ferritin; 1.
DR ProDom; PD000971; Ferritin; 1.
DR PROSITE; PS00540; FERRITIN_1; FALSE_NEG.
DR PROSITE; PS00204; FERRITIN_2; 1.
DR PROSITE; PS0905; FERRITIN LIKE; 1.
KW Direct protein sequencing; Iron; Iron storage; Metal-binding.
FT INIT MET 0 0 By similarity
FT DOMAIN 10 159 Ferritin-like diiron.
FT METAL 27 27 Iron (By similarity).
FT METAL 61 61 Iron (By similarity).
FT METAL 62 62 Iron (By similarity).
FT METAL 65 65 Iron (By similarity).
FT METAL 107 107 Iron (By similarity).
FT METAL 141 141 Iron (By similarity).
FT CONFLICT 78 78 A -> G (in Ref. 2).
SQ SEQUENCE 170 AA; 19931 MW; 32FD337E11F16FD0 CRC64;

Query Match 62.8%; Score 560.5; DB 1; Length 170;
Best Local Similarity 78.9%; Pred. No. 3.1e-42;
Matches 112; Conservative 6; Mismatches 11; Indels 13; Gaps 2;

Qy 2 TTASTQVRQNYHQDSEAAINRQINLELYASVYVLSMSYFFDRDDVALKNFAKYFLHQSH 61
Db 1 TTASTQVRQNYHQDSEAAINRQINLELYASVYVLSMSYFFDRDDVALKNFAKYFLHQSH 60

Qy 62 EERQHAELMKLQNGRGRIFLQDIKKPDCDDWESGLNAMECALHLEKNVNSLLEFPSP 121
Db 61 EEREHAERLMKLQNGRGRIFLQDIKKPDRDDWENGLNAMECALCLERSVNSQLLEL--- 117

Qy 122 ISPSFSCWHYTTNRPQPQHLL 143
Db 118 -----HKLATEKNDP--HL 129
```

Search completed: March 30, 2005, 19:42:13  
Job time : 182 secs

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GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: March 30, 2005, 19:30:30 ; Search time 72 Seconds  
(without alignments)  
886.326 Million cell updates/sec

Title: US-09-786-867C-5  
Perfect score: 893  
Sequence: 1 MTTASTSQVRQNYHDSAA.....PARRKRPHSIPTPIIFRSP 165

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:.\*  
1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	881	98.7	165	3 AAY53271	Human onc
2	615.5	68.9	183	2 AAR71567	Aar71567 Human mon
3	615.5	68.9	183	4 AAB90804	Aab90804 Human she
4	615.5	68.9	183	7 ADD22444	Add22444 HLA-B46 T
5	615.5	68.9	183	7 ADI15887	Adi15887 Human pp
6	615.5	68.9	183	8 ABM81295	Abm81295 Tumour-as
7	615.5	68.9	190	7 ADG42360	Adg42360 Ferritin
8	615.5	68.9	190	8 ADQ29701	Adq29701 Human col
9	615.5	68.9	190	8 ADP24691	Adp24691 PRO polyyp
10	615.5	68.9	206	5 ABB97273	Abb97273 Novel hum
11	615.5	68.9	222	6 ABR41768	Abra41768 Human DIT
12	615.5	68.9	362	8 ADQ82746	Adq82746 Recombina
13	610.5	68.4	183	7 ADN31067	Adn31067 Human H-c
14	580.5	65.0	180	5 ABP69305	Abp69305 Human pol
15	580.5	65.0	182	4 AAU27741	Aau27741 Mouse ful
16	580.5	65.0	227	6 ABU11456	Abu11456 Human MDD
17	579	64.8	165	8 ABM81021	Abm81021 Tumour-as
18	540	60.5	148	4 AAO04400	Aao04400 Human pol
19	523.5	58.6	127	5 ABP42274	Abp42274 Human ova
20	494	55.3	242	5 ABG32428	Abg32428 Human sec
21	477	53.4	173	4 AAB09630	Aab09630 Human gen
22	477	53.4	173	7 ADG62935	Adg62935 Novel hum
23	424.5	47.5	146	8 ABM80602	Abm80602 Tumour-as
24	421.5	47.2	373	8 ABM80723	Abm80723 Tumour-as
25	421	47.1	621	4 ABG28304	Abg28304 Novel hum

## ALIGNMENTS

## RESULT 1

AA53271  
ID AAY53271 standard; protein; 165 AA.

XX AC AAY53271;

XX DT 20-JUL-2000 (first entry)

XX DE Human oncofoetal ferritin 1 protein sequence.

XX KW Human; oncofoetal ferritin 1; OFF1; ferritin; transplacental;  
XX KW pathological pregnancy; breast cancer; cytostatic; immunosuppressive;  
XX KW contraceptive; abortive; nontropic; vaccine; immunisation; cancer;  
XX KW transplant rejection; autoimmune disease; fertilisation; diagnosis;  
XX KW in vitro fertilization; IVF; hepatoblastoma; Hodgkin's lymphoma;  
XX KW leukaemia; non-Hodgkin's lymphoma; embryonal tumour; Down's Syndrome;  
XX KW spontaneous abortion; miscarriage; premature contraction; toxemia;  
XX KW premature delivery.

XX OS Homo sapiens.

XX PN WO200015788-A2.

XX PD 23-MAR-2000.

XX XX 08-SEP-1999; 99WO-IL000485.

XX XX 11-SEP-1998; 98IL-00126181.

XX XX (GARD-) GARDINO INVESTMENT NV.

XX XX Moroz C;

XX WPI; 2000-271427/23.

XX N-PSDB; AAA13647.

XX DNA sequence coding for oncofetal ferritin 1 protein, useful for

XX immunisations against breast cancer, for enhancing fertilization rates

XX during in vitro fertilization treatment and for use as a growth factor of

XX bone-marrow progenitor cells.

XX Example 7; Fig 5; 60pp; English.

XX The present sequence represents the human oncofetal ferritin 1 (OFF1)  
XX protein. OFF1 has cytostatic, immunosuppressive, contraceptive, abortive  
XX and nontropic activities, and can be used as a vaccine. Compositions  
XX comprising the expression vector containing an OFF1 coding sequence, and  
XX the OFF1 protein, are useful: (a) for immunisations against cancer,

26 416.5 46.6 275 4 ABG21478 Novel hum  
27 399 44.7 183 4 AAU07890 Polypepti  
28 399 44.7 183 7 ADG84955 Cancer-as  
29 399 44.7 713 4 ABG12069 Novel hum  
30 399 44.7 713 4 ABG07849 Novel hum  
31 395.5 44.3 144 8 ADO43747 Amino aci  
32 392 43.9 183 6 ABR82317 Human met  
33 392 43.9 201 4 ABG27400 Novel hum  
34 390.5 43.7 183 5 ABU65170 Human NOV  
35 390.5 43.7 183 8 ADN61991 Human nov  
36 390.5 43.7 317 7 ADC31487 Human nov  
37 387.5 43.4 204 6 ABB99663 Amino aci  
38 379.5 42.5 178 8 ABO59224 Human gen  
39 379 42.4 248 4 ABG27399 Novel hum  
40 377 42.2 141 4 ABG17463 Novel hum  
41 375.5 42.0 221 4 AAU07889 Polypepti  
42 361 40.4 85 3 AAB58474 Lung canc  
43 343 38.4 199 5 ABP51378 Human MDD  
44 324.5 36.3 153 6 ABU70932 Human adi  
45 316 35.4 175 6 ABR64209 Angiogene

CC especially breast cancer; (b) in the treatment of transplant rejections,  
 CC autoimmune diseases, pathological pregnancies; (c) for enhancing  
 CC fertilisation rates during in vitro fertilisation (IVF) treatment; and  
 CC (d) for use as a growth factor of bone-marrow progenitor cells such as  
 CC granulocyte monocytes. The OFF1 nucleotide sequence is useful for  
 CC diagnosing cancer such as breast cancer, hepatoblastoma, leukaemia,  
 CC Hodgkin's and non-Hodgkin's lymphomas and embryonal tumours, Down's  
 CC Syndrome, and pathological pregnancies such as spontaneous abortion and  
 CC miscarriage, premature contractions, toxemia or premature delivery  
 XX Sequence 165 AA;

Query Match 98.7%; Score 881; DB 3; Length 165;  
 Best Local Similarity 98.8%; Pred. No. 6.4e-90;  
 Matches 163; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTTASTSQVRQNYHODSEAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHQ 60  
 DB 1 MTTASTSQVRQNYHODSEAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHQ 60  
 QY 61 HEERQHAELKMLQNGRGRIFLODIKKPDCDDWESGLNAMECALHLEKNVNSLLEPPS 120  
 DB 61 HEERQHAELKMLQNGRGRIFLODIKKPDCDDWESGLNAMECALHLEKNVNSLLEPPS 120  
 QY 121 PISPSPCSWHHYTTNRPOQHLLRPRRKRPHSIPTPIILFRSP 165  
 DB 121 PISPSPCSWHHYTTNRPEQHLLRPRRKRPHSIPTPIILFRSP 165

RESULT 2  
 AAR71567  
 ID AAR71567 standard; protein; 183 AA.  
 AC AAR71567;  
 XX 01-NOV-1995 (first entry)  
 DT Human monocyte growth factor.  
 DE Monocyte growth factor; human; lung; cancer cell line;  
 KW cellular immune function; macrophage.  
 KW Homo sapiens.  
 OS JP07031482-A.  
 PN 03-FEB-1995.  
 PD 21-JUL-1993; 93JP-00200129.  
 PF 21-JUL-1993; 93JP-00200129.  
 PR 21-JUL-1993; 93JP-00200129.  
 XX (LIPE-) ZH LIFE TECHNOLOGY KENKYUSHO.  
 PA WPI: 1995-109536/15.  
 DR N-PSDB; AAQ85979.  
 XX Recombinant human monocyte growth factor and its coding DNA - useful for  
 PT stimulation of cellular immune function and macrophage.  
 PT Claim 1; Page 2; 12pp; Japanese.  
 PS The amino acid sequence of a novel monocyte growth factor. The protein  
 CC was isolated from a human lung cancer cell line, T3M-30Lu (FERM BP3120).  
 CC The sequence of the protein was determined by amino acid sequencing  
 CC following cleavage of the purified protein by V8 protease. The gene  
 CC encoding this protein can be used to produce recombinant monocyte growth  
 CC factor which can be used for stimulation of cellular immune function and  
 CC macrophages  
 XX Sequence 183 AA;

Query Match 68.9%; Score 615.5; DB 2; Length 183;  
 Best Local Similarity 84.6%; Pred. No. 3.7e-60;  
 Matches 121; Conservative 3; Mismatches 6; Indels 13; Gaps 2;

QY 1 MTTASTSQVRQNYHODSEAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHQ 60  
 DB 1 MTTASTSQVRQNYHODSEAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHQ 60  
 QY 61 HEERQHAELKMLQNGRGRIFLODIKKPDCDDWESGLNAMECALHLEKNVNSLLEPPS 120  
 DB 61 HEERQHAELKMLQNGRGRIFLODIKKPDCDDWESGLNAMECALHLEKNVNSLLEPPS 120

Best Local Similarity 84.6%; Pred. No. 3.7e-60;  
 Matches 121; Conservative 3; Mismatches 6; Indels 13; Gaps 2;

QY 1 MTTASTSQVRQNYHODSEAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHQ 60  
 DB 1 MTTASTSQVRQNYHODSEAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHQ 60  
 QY 61 HEERQHAELKMLQNGRGRIFLODIKKPDCDDWESGLNAMECALHLEKNVNSLLEPPS 120  
 DB 61 HEERQHAELKMLQNGRGRIFLODIKKPDCDDWESGLNAMECALHLEKNVNSLLEPPS 120  
 QY 121 PISPSPCSWHHYTTNRPOQHLL 143  
 DB 119 -----HKLATDKNDP--HL 130

RESULT 3  
 AAB90804  
 ID AAB90804 standard; protein; 183 AA.  
 AC AAB90804;  
 XX 15-JUN-2001 (first entry)  
 DT Human shear stress-response protein SEQ ID NO: 108.  
 DE Human; shear stress-response protein; vascular disease; arteriosclerosis.  
 KW Homo sapiens.  
 OS WO200125427-A1.  
 PN 12-APR-2001.  
 PD 02-OCT-2000; 2000WO-JP006840.  
 PF 01-OCT-1999; 99JP-00280976.  
 PR (KYOW) KYOWA HAKKO KOGYO KK.  
 PA (NOJII) NOJIMA H.  
 XX Nojima H, Yoshisue H, Obayashi M, Ota T, Kawabata A, Sakurada K;  
 PI Kuga T, Sekine S, Nakamura Y, Sugano S;  
 XX WPI: 2001-266308/27.  
 DR N-PSDB; AAH02927.  
 XX DNA sequences, proteins encoded by them and antibodies against them  
 PT useful in diagnosis and treatment of vascular disease caused by  
 PT arteriosclerosis.  
 XX Claim 60; Page 539-540; 678pp; Japanese.  
 PS The present invention provides the protein and coding sequences of a  
 CC number of human shear stress response proteins. These are useful in the  
 CC diagnosis, treatment and screening of vascular diseases caused by  
 CC arteriosclerosis, including heart failure, post-PTCA restenosis and  
 CC hypertension  
 XX Sequence 183 AA;

Query Match 68.9%; Score 615.5; DB 4; Length 183;  
 Best Local Similarity 84.6%; Pred. No. 3.7e-60;  
 Matches 121; Conservative 3; Mismatches 6; Indels 13; Gaps 2;

QY 1 MTTASTSQVRQNYHODSEAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHQ 60  
 DB 1 MTTASTSQVRQNYHODSEAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHQ 60  
 QY 61 HEERQHAELKMLQNGRGRIFLODIKKPDCDDWESGLNAMECALHLEKNVNSLLEPPS 120  
 DB 61 HEERQHAELKMLQNGRGRIFLODIKKPDCDDWESGLNAMECALHLEKNVNSLLEPPS 120



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OY 121 PISPSPCWHYTTNRPOQHHL 143
DB 119 -----HKLATDKNDP--HL 130

RESULT 4
ADD22444
ID ADD22444 standard; protein; 183 AA.
XX
AC ADD22444;
XX
DT 15-JAN-2004 (first entry)
XX
DE HLA-B46 T cell recognised tumour antigenic polypeptide, SEQ No 94.
XX
KW tumour antigenic peptide; cancer; vaccine; cytostatic; cytotoxic T cell;
KW colon; mouth; lung; prostatic; gynecological; human.
XX
OS Homo sapiens.
XX
PN JP2003111595-A.
XX
PD 15-APR-2003.
XX
PF 24-JUN-2002; 2002JP-00183603.
XX
PR 25-JUN-2001; 2001JP-00191974.
XX
PA (ITOY/) ITO Y.
XX
DR WPI; 2003-611129/58.
XX
PT Novel tumor antigenic peptide or polypeptide useful for inducing
PT cytotoxic T cells or for treating cancer such as colon, mouth, lung,
PT prostatic or gynecological cancer.
XX
PS Claim 2; SEQ ID NO 94; 98pp; Japanese.
XX
CC The invention relates to a novel tumour antigenic peptide or polypeptide
CC comprising a sequence selected from 99 sequences fully defined in the
CC specification. The tumour antigenic peptide or polypeptide comprises a
CC sequence selected from 99 sequences fully defined in the specification,
CC where the tumour antigenic peptide preferably has a sequence of Glu-Pro-
CC pro-Leu-Ser-Gln-Glu-Thr-Phe, and the polypeptide preferably has a
CC sequence comprising 393 amino acids fully defined in the specification.
CC The invention further provides a cancer vaccine comprising a tumour
CC antigenic peptide or polypeptide, which has cytostatic activity. A tumour
CC hybridising polynucleotide, a recombinant vector containing the
CC polynucleotide, a host transformed with the vector or an antibody are
CC useful for screening for compounds that interact with the tumour
CC antigenic peptide, the polypeptide or its encoding polynucleotide and
CC increases the expression of the tumour antigenic peptide, the polypeptide
CC or polynucleotide. The tumour antigenic peptide or the polypeptide is
CC useful for inducing cytotoxic T cells. The tumour antigenic peptide
CC vaccine is useful for treating cancer such as colon, mouth, lung,
CC prostatic or gynecological cancer. The invention also provides a
CC pharmaceutical composition useful for treating cancer. The tumour
CC antigenic peptide or the polypeptide is useful as an antigen to create
CC antibodies. This sequence represents one of the tumour antigenic
CC polypeptides of the invention.
XX
SQ Sequence 183 AA;
Query Match 68.9%; Score 615.5; DB 7; Length 183;
Best Local Similarity 84.6%; Pred. No. 3.7e-60;
Matches 121; Conservative 3; Mismatches 6; Indels 13; Gaps 2;

OY 1 MTTASTSQVRQNYHQDSEAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYLHQHS 60
DB 1 MTTASTSQVRQNYHQDSEAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYLHQHS 60
OY 61 HEERQHAELKMLQNGRGRIFLODIKKPCDDWESGLNAMECALHLEKNVNSLLEL-- 120
DB 61 HEERQHAELKMLQNGRGRIFLODIKKPCDDWESGLNAMECALHLEKNVNSLLEL-- 118
OY 121 PISPSPCWHYTTNRPOQHHL 143
DB 119 -----HKLATDKNDP--HL 130

RESULT 5
ADI15887
ID ADI15887 standard; protein; 183 AA.
XX
AC ADI15887;
XX
DT 22-APR-2004 (first entry)
XX
DE Human PP 84.
XX
KW tumour; antigen; human leukocyte antigen; HLA-A2; HLA-A26;
KW cytotoxic T-cell; CTL; vaccine; cancer; colorectal cancer;
KW stomach cancer; buccal cancer; renal cancer; lung cancer;
KW gynecological cancer; prostate cancer.
XX
OS Homo sapiens.
XX
PN WO2003008450-A1.
XX
PD 30-JAN-2003.
XX
PF 11-JUN-2002; 2002WO-JP005799.
XX
PR 12-JUN-2001; 2001JP-00177058.
PR 21-AUG-2001; 2001JP-00250728.
XX
PA (ITOH/) ITOH K.
XX
PI Itoh K, Shichijo S;
XX
DR WPI; 2003-267996/26.
DR N-PSDB; ADI15962.
XX
PT Tumor antigen peptides recognized by human leukocyte antigen (HLA)-A2 or
PT HLA-A26 restricted cytotoxic T-cells for treatment and prevention of
PT cancer including preparation of cancer vaccines.
XX
PS Claim 2; SEQ ID NO 231; 323pp; Japanese.
XX
CC The invention relates to a tumour antigen peptide recognised by human
CC leukocyte antigen (HLA)-A2 or HLA-A26 restricted cytotoxic T-cells (CTL)
CC and/or capable of inducing CTL. The tumour antigen peptide is useful for
CC the treatment, prevention, diagnosis and vaccine production for cancers
CC including colorectal, stomach, buccal, renal, lung, gynecological and
CC prostate cancer. The present sequence represents the amino acid sequence
CC of a human protein.
XX
SQ Sequence 183 AA;
Query Match 68.9%; Score 615.5; DB 7; Length 183;
Best Local Similarity 84.6%; Pred. No. 3.7e-60;
Matches 121; Conservative 3; Mismatches 6; Indels 13; Gaps 2;

OY 1 MTTASTSQVRQNYHQDSEAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYLHQHS 60
DB 1 MTTASTSQVRQNYHQDSEAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYLHQHS 60
OY 61 HEERQHAELKMLQNGRGRIFLODIKKPCDDWESGLNAMECALHLEKNVNSLLEL-- 120
DB 61 HEERQHAELKMLQNGRGRIFLODIKKPCDDWESGLNAMECALHLEKNVNSLLEL-- 118
OY 121 PISPSPCWHYTTNRPOQHHL 143
DB 119 -----HKLATDKNDP--HL 130

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QY	61	HEERQHAELKMLQNRGGRIFLQDIKKPDCDDWESGLNAMECALHLEKNVNOSLLEFPS	12
DB	61	HEERHAEKMLQNRGGRIFLQDIKKPDCDDWESGLNAMECALHLEKNVNOSLLEL	118
QY	121	PISPPSCWHYTTNRPPQHLL	143
DB	119	-----HKLATDKNDP--HL	130
RESULT 7			
ID	ADG42360		
XX	ID	ADG42360 standard; peptide; 190 AA.	
AC	ADG42360;		
XX	XX	26-FEB-2004 (first entry)	
DT	XX	Ferritin H chain for fusion protein construction.	
DE	XX	anti-HIV; virucide; vaccine; gene therapy; ferritin; fusion protein;	
XX	XX	polymeric assembly; AIDS; SARS; oxygen transport; blood substitute;	
KW	KW	image contrast agent; metal chelating agent; gelling agents;	
KW	KW	protein purification platform.	
XX	XX	Homo sapiens.	
OS	XX	WO2003094849-A2.	
XX	XX	20-NOV-2003.	
PD	XX	12-MAY-2003; 2003WO-US014617.	
PF	XX	10-MAY-2002; 2002US-0379145P.	
XX	XX	(NEWC-) NEW CENTURY PHARM INC.	
PR	XX	Carter DC, Li CQ;	
XX	XX	WPI; 2003-903936/82.	
DR	XX	New ferritin fusion proteins in which ferritin is fused with a protein	
XX	XX	capable of being fused to ferritin without interfering with polymeric	
PT	XX	assembly of resulting fusion protein, useful as human or veterinary	
PT	XX	vaccines and therapeutics.	
PS	XX	Disclosure; SEQ ID NO 8; 52pp; English.	
XX	XX	The invention relates to a ferritin fusion protein comprising a fusion	
CC	XX	protein selected from a ferritin protein fused at the C-terminus or at	
CC	XX	the N-terminus with a protein or peptide capable of being fused to	
CC	XX	ferritin without interfering with the polymeric assembly of the resulting	
CC	XX	fusion protein. The fusion proteins are useful in the development of	
CC	XX	human and veterinary vaccines and therapeutics against e.g. AIDS or SARS,	
CC	XX	or in other applications including oxygen transport and the therapeutic	
CC	XX	delivery of drugs and other therapeutic agents, or as blood substitutes,	
CC	XX	image contrast agents, metal chelating agents, gelling agents, protein	
CC	XX	purification platforms, and therapeutic receptor-binding proteins. In	
CC	XX	examples of the invention, the ferritin H chain is fused to a number of	
CC	XX	proteins via Gly spacer. This sequence represents the ferritin H chain	
CC	XX	which is fused to a number of peptides/proteins.	
XX	XX	Sequence 190 AA;	
QY	1	MTTASTSQVRNQHODSEAAINRQINLELYASVYVLSMSYFDRDDVALKNFAKYLHQS	60
DB	1	MTTASTSQVRNQHODSEAAINRQINLELYASVYVLSMSYFDRDDVALKNFAKYLHQS	60
QY	61	HEERQHAELKMLQNRGGRIFLQDIKKPDCDDWESGLNAMECALHLEKNVNOSLLEFPS	120

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Db      61 HEERHAEKMKLQNGRGRIFLODIKKPCDDWESGLNAMECALHLEKNVNSLLEL-- 118
QY      121 PISPSPSCWHHYTTNRPOQHHL 143
Db      119 -----HKLATDKNDP--HL 130

RESULT 8
ADQ29701
XX      ID      ADQ29701 standard; protein; 190 AA.
XX      AC      ADQ29701;
XX      DT      07-OCT-2004 (first entry)
XX      DE      Human colorectal cancer-associated protein #56.
XX      KW      human; colon cancer; TIMP1; Regl-alpha;
XX      KW      colorectal cancer-associated marker.
XX      OS      Homo sapiens.
XX      PN      EP1439393-A2.
XX      PD      21-JUL-2004.
XX      PP      15-DEC-2003; 2003EP-00257868.
XX      PR      13-DEC-2002; 2002US-0433554P.
XX      PR      31-JUL-2003; 2003US-0491397P.
XX      PR      (FARB ) BAYER HEALTHCARE LLC.
XX      PR      (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
XX      PI      Astle JH, Boardman LA, Bugart LJ, Burgess CC, Catino TJ,
XX      PI      Dwivedi P, Huntress M, Johnson KA, Lewis ME, Maimonis PJ,
XX      PI      Brown-Shimer SLA, Thiagalingam A, Thibodeau SN, Molino GA;
XX      PI      WPI; 2004-545561/53.
XX      DR      N-PSDB; ADQ29634.
XX      PT      Diagnosing colon cancer in individual, preferably human, by detecting
XX      PT      presence of TIMP 1 in sample, where presence of TIMP 1 in sample is
XX      PT      indicative of colon cancer in individual.
XX      PS      Claim 7; SEQ ID NO 127; 433pp; English.
XX      CC      The invention comprises a method for diagnosing colon cancer in an
XX      CC      individual, the method involves obtaining a serum sample from the
XX      CC      individual and detecting the presence of either TIMP1 or Regl-alpha and
XX      CC      an additional colorectal cancer-associated marker. The method of the
XX      CC      invention is useful for diagnosing colon cancer in an individual. The
XX      CC      present amino acid sequence represents a human colorectal cancer-
XX      CC      associated protein of the invention.
XX      SQ      Sequence 190 AA;
XX      Query Match      68.9%; Score 615.5; DB 8; Length 190;
XX      Best Local Similarity      84.6%; Pred. No. 3.9e-60;
XX      Matches 121; Conservative      3; Mismatches      6; Indels      13; Gaps      2

QY      1      MTTASTSOVRONYHODSEAAINROINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHOS 60
Db      1      MTTASTSOVRONYHODSEAAINROINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHOS 60
QY      61 HEERHAEKMKLQNGRGRIFLODIKKPCDDWESGLNAMECALHLEKNVNSLLEPFS 120
Db      61 HEERHAEKMKLQNGRGRIFLODIKKPCDDWESGLNAMECALHLEKNVNSLLEL-- 118

QY      121 PISPSPSCWHHYTTNRPOQHHL 143
Db      119 -----HKLATDKNDP--HL 130

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Matches 121; Conservative 3; Mismatches 6; Indels 13; Gaps 2;

QY 1 MTTASTSQVRQYHDSAAINRQINLELYASVYVLSMSYFDRDDVALKNFAKYFLHQS 60  
 Db 1 MTTASTSQVRQYHDSAAINRQINLELYASVYVLSMSYFDRDDVALKNFAKYFLHQS 60

QY 61 HEERQHAELKMLQNGRGRIFLODIKKPDCDDWESGLNAMECALHLEKNVNSLLEPPS 120  
 Db 61 HEERQHAELKMLQNGRGRIFLODIKKPDCDDWESGLNAMECALHLEKNVNSLLEPPS 120

QY 121 PISPSPCWHYHTNRPQPHL 143  
 Db 119 -----HKLATDKNDP--HL 130

RESULT 10  
 ABB97273  
 ID ABB97273 standard; protein; 206 AA.

AC ABB97273;  
 XX  
 DT 27-JUN-2002 (first entry)  
 XX  
 DE Novel human protein SEQ ID NO: 541.  
 XX  
 KW Human; antianemic; vulnary; antiinflammatory; immunomodulator;  
 KW antifertility; cerebroprotective; cytostatic; rheumatic; gene therapy;  
 KW neuroprotective; antiparkinsonian; protein therapy; EST;  
 KW expressed sequence tag.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200222660-A2.  
 XX  
 PD 21-MAR-2002.  
 XX  
 PF 10-SEP-2001; 2001WO-US026015.  
 XX  
 PR 11-SEP-2000; 2000US-00659671.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;  
 PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;  
 XX  
 DR WPI; 2002-292408/33.  
 DR N-PSDB; AEN32459.

An isolated polynucleotide for treating diseases associated with its encoded polypeptide such as cancer and multiple sclerosis.

Example 2; SEQ ID NO 541; 509pp; English.

The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTs). They can be used to stimulate cell growth, to regulate haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. Parkinson's disease. The present sequence is a protein of the invention

Sequence 206 AA;

Query Match 68.9%; Score 615.5; DB 5; Length 206;

Best Local Similarity 84.6%; Pred. No. 4.3e-60;

Matches 121; Conservative 3; Mismatches 6; Indels 13; Gaps 2;

QY 1 MTTASTSQVRQYHDSAAINRQINLELYASVYVLSMSYFDRDDVALKNFAKYFLHQS 60  
 Db 24 MTTASTSQVRQYHDSAAINRQINLELYASVYVLSMSYFDRDDVALKNFAKYFLHQS 83

QY 61 HEERQHAELKMLQNGRGRIFLODIKKPDCDDWESGLNAMECALHLEKNVNSLLEPPS 120  
 Db 84 HEERQHAELKMLQNGRGRIFLODIKKPDCDDWESGLNAMECALHLEKNVNSLLEPPS 141

QY 121 PISPSPCWHYHTNRPQPHL 143  
 Db 142 -----HKLATDKNDP--HL 153

RESULT 11  
 ABR41768  
 ID ABR41768 standard; protein; 222 AA.

AC ABR41768;  
 XX  
 DT 02-JUN-2003 (first entry)  
 XX  
 DE Human DITHP biochemical pathway protein.  
 XX  
 KW Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;  
 KW cancer; cell proliferative disorder; autoimmune disorder;  
 KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;  
 KW neurological disorder; gastrointestinal disorder; transport disorder;  
 KW connective tissue disorder; drug screening; proteome analysis;  
 KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;  
 KW disease model; toxicological testing; transcript imaging;  
 KW biochemical pathway.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200297031-A2.  
 XX  
 PD 05-DEC-2002.  
 XX  
 PF 27-MAR-2002; 2002WO-US010056.  
 XX  
 PR 28-MAR-2001; 2001US-0279619P.  
 PR 29-MAR-2001; 2001US-0280067P.  
 PR 29-MAR-2001; 2001US-0280068P.  
 PR 16-MAY-2001; 2001US-0291280P.  
 PR 17-MAY-2001; 2001US-0291829P.  
 PR 17-MAY-2001; 2001US-0291849P.  
 PR 19-JUN-2001; 2001US-0299428P.  
 PR 20-JUN-2001; 2001US-0299776P.  
 PR 20-JUN-2001; 2001US-0300001P.  
 XX  
 PA (INCY-) INCYTE GENOMICS INC.

PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;  
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshay SR;  
 PI Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;  
 PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;  
 PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;  
 XX  
 DR WPI; 2003-129518/12.  
 DR N-PSDB; ACC46705.

Novel human diagnostic and therapeutic polypeptide useful for identifying test compound which specifically binds to a polypeptide encoded by human diagnostic and therapeutic polynucleotide, and to induce antibodies.

Claim 27; SEQ ID NO 1303; 591pp; English.

The invention relates to novel human diagnostic and therapeutic polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded proteins (DITHP; ABR41136-ABR41812). The invention also relates to polynucleotide sequences at least 90% identical to the dithp cDNA sequences of the invention; recombinant vectors, host cells and transgenic organisms comprising a dithp nucleic acid sequence; the recombinant production of DITHP proteins; antibodies specific for DITHP proteins; microarrays comprising dithp nucleic acid sequences; methods of detecting dithp nucleotide and protein sequences; methods of screening

CC for compounds which specifically bind a DITHP protein; and methods of  
 CC assessing the toxicity of test compounds using a dithp hybridisation  
 CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the  
 CC diagnosis of a wide variety of conditions including cancer and other cell  
 CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,  
 CC viral, fungal or parasitic infections; hormonal disorders; metabolic  
 CC disorders; neurological disorders; gastrointestinal disorders; transport  
 CC disorders; and connective tissue disorders. They may also be used to  
 CC screen for modulators of protein activity or gene expression. DITHP  
 CC proteins can additionally be used in analysis of the proteome of a tissue  
 CC or cell type and to induce antibodies. The dithp nucleic acids are  
 CC additionally useful in somatic or germline gene therapy of the disorders  
 CC mentioned above, as a source of antisense sequences, as a source of  
 CC probes and primers, in genotyping and identification of individuals, in  
 CC the generation of transgenic animal models of human disease or knock in  
 CC humanised animals, in toxicological testing, and in transcript imaging.  
 CC The present sequence represents a DITHP protein which is involved in a  
 CC biochemical pathway. Note: The sequence data for this patent did not form  
 CC part of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 CC  
 CC Sequence 222 AA;

Query Match 68.9%; Score 615.5; DB 6; Length 222;  
 Best Local Similarity 84.6%; Pred. No. 4.8e-60;  
 Matches 121; Conservative 3; Mismatches 6; Indels 13; Gaps 2;  
 QY 1 MTTASTSVQRNYHDSAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYFLHQS 60  
 DB 28 MTTASTSVQRNYHDSAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYFLHQS 87  
 QY 61 HEERHAEKMKLQNGRGRIFLDIKKPDCCDDWESGLNAMECALHLEKNVNSLLEPPS 120  
 DB 88 HEERHAEKMKLQNGRGRIFLDIKKPDCCDDWESGLNAMECALHLEKNVNSLLEPPS 145  
 QY 121 PISPSPSCWHYTTNRPOQHHL 143  
 DB 146 -----HKLATDKNDP--HL 157

RESULT 12  
 ADQ82746  
 ID ADQ82746 standard; protein; 362 AA.  
 AC ADQ82746;  
 DT 09-SEP-2004 (first entry)  
 DE Recombinant human ferritin protein.  
 KW human; ferritin protein.  
 XX Homo sapiens.  
 XX KR2004007892-A.  
 XX 28-JAN-2004.  
 XX 11-JUL-2002; 2002KR-00040497.  
 XX 11-JUL-2002; 2002KR-00040497.  
 XX (BIOP-) BIOPROGEN CO LTD.  
 XX Ham MS, Jung BH, Kim SU, Lee EG, Lee JW;  
 XX WPI; 2004-386312/36.  
 XX DR N-PSDB; ADQ82747.  
 XX New recombinant human ferritin proteins and production method of them.  
 PS Claim 8; SEQ ID NO 11; 27pp; Korean.

CC The invention comprises the amino acid and coding sequences of a  
 CC recombinant human ferritin protein, the invention also comprises a  
 CC production method for the recombinant human ferritin protein. The present  
 CC amino acid sequence represents the recombinant human ferritin protein of  
 CC the invention.  
 CC Sequence 362 AA;

Query Match 68.9%; Score 615.5; DB 8; Length 362;  
 Best Local Similarity 84.6%; Pred. No. 9.5e-60;  
 Matches 121; Conservative 3; Mismatches 6; Indels 13; Gaps 2;  
 QY 1 MTTASTSVQRNYHDSAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYFLHQS 60  
 DB 1 MTTASTSVQRNYHDSAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYFLHQS 60  
 QY 61 HEERHAEKMKLQNGRGRIFLDIKKPDCCDDWESGLNAMECALHLEKNVNSLLEPPS 120  
 DB 61 HEERHAEKMKLQNGRGRIFLDIKKPDCCDDWESGLNAMECALHLEKNVNSLLEPPS 118  
 QY 121 PISPSPSCWHYTTNRPOQHHL 143  
 DB 119 -----HKLATDKNDP--HL 130

RESULT 13  
 ADN31067  
 ID ADN31067 standard; protein; 183 AA.  
 AC ADN31067;  
 DT 17-JUN-2004 (first entry)  
 DE Human H-chain ferritin (rHN) protein.  
 KW human; H-chain ferritin; rHN; anaemia; iron.  
 XX Homo sapiens.  
 XX KR2002090036-A.  
 XX 30-NOV-2002.  
 XX 25-MAY-2001; 2001KR-00029187.  
 XX 25-MAY-2001; 2001KR-00029187.  
 XX (JUNG/) JUNG J M.  
 XX Jung JM, Lee YJ;  
 XX WPI; 2003-339039/32.  
 XX DR N-PSDB; ADN31064.  
 XX Overexpression method of recombinant human h-chain ferritin in Pichia  
 XX pastoris and therapeutic composition for anemia using the same.  
 XX Disclosure; Page 11; 13pp; Korean.  
 XX This invention relates to the novel overexpression production of  
 XX recombinant human H-chain ferritin (rHN) in Pichia pastoris (P.  
 XX pastoris). Specifically, it refers to the development of pharmaceutical  
 XX compositions for the treatment of anaemia, due to the excellent capacity  
 XX of this protein for storing iron. The present invention describes  
 XX recombinant Pichia pastoris obtained by transformation using an  
 XX expression vector pGAP2 alpha A/rHN derived from Pichia pastoris and  
 XX containing human H-chain ferritin (rHN) gene. The human recombinant rHN  
 XX is a homopolymer consisting of 24 H-chains having 24000 Da and its  
 XX molecular weight is 576000 Da. This polypeptide sequence is the human H-  
 XX chain ferritin protein of the invention.  
 XX Sequence 183 AA;



PS Claim 10; SEQ ID NO 238; 153pp; English.  
XX Sequences AAU27676-AAU28019 represent full-length polypeptides and contig  
CC polypeptides of the invention. The proteins and their associated DNA  
CC sequences are useful for the treatment, diagnosis and prevention of  
CC various types of disorder in a mammalian subject such as a human, dog,  
CC monkey, mouse, hamster or rat. The disorders include cancers such as  
CC leukaemia, lymphoma and neuroblastoma, autoimmune disorders such as  
CC multiple sclerosis, connective tissue disease, rheumatoid arthritis,  
CC diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system  
CC disorders such as Parkinson's disease, Alzheimer's disease, Huntington's  
CC chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and  
CC Wernicke disease, inflammatory disorders such as nephritis, Crohn's  
CC disease, ischaemia-reperfusion injury, shock, sepsis and inflammatory  
CC bowel disease. The sequences exhibit activity relating to angiogenesis,  
CC cell proliferation, cell differentiation, stem cell growth factor,  
CC activin or inhibin. Therefore, they can be used to manipulate stem cells  
CC in culture to give rise to neuroepithelial cells that can be used to  
CC augment or replace cells damaged by illness, accidental damage or genetic  
CC disorders. The sequences may also be used for regeneration of bone,  
CC cartilage, tendons and ligaments and in tissue repair and burn healing.  
CC Note: Some sequences for this patent did not form part of the printed  
CC specification, but were obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX SQ Sequence 182 AA;

Query Match 65.0%; Score 580.5; DB 4; Length 182;  
Best Local Similarity 81.1%; Pred. No. 3e-56;  
Matches 116; Conservative 5; Mismatches 9; Indels 13; Gaps 2;  
Qy 1 MTTASTSQVRQNYHODSEAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYFLHQ 60  
Db 1 MTTASPSQVRQNYHODSEAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYFLHQ 60  
Qy 61 HEEROHAELMKLQNRGRIFLDI KKPDCDDWESGLNAMECALHLEKNVNSLLEPPS 120  
Db 61 HEEROHAELMKLQNRGRIFLDI KKPDCDDWESGLNAMECALHLEKNVNSLLEPPS 118  
Qy 121 PISPSPCWHYTTNRPOPHHL 143  
Db 119 -----HKLATDKNDP--HL 130

Search completed: March 30, 2005, 19:39:12  
Job time : 80 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 30, 2005, 19:37:13 ; Search time 16 Seconds  
(Without alignments)  
992.235 Million cell updates/sec

Title: US-09-786-867C-5

Perfect score: 893

Sequence: 1 MTTASTSQVRQNYHQDSEA.....PRRRKRPHSIPTPIIRSP 165

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	615.5	68.9	183	1 FRHUH	ferritin heavy cha
2	580.5	65.0	141	2 I48109	ferritin heavy cha
3	580.5	65.0	182	2 S06070	ferritin heavy cha
4	573.5	64.2	181	2 A39884	ferritin heavy cha
5	560.5	62.8	180	2 A26886	ferritin heavy cha
6	499.5	55.9	164	2 I46710	ferritin heavy cha
7	439	49.2	174	2 S45603	ferritin, soma - g
8	424.5	47.5	176	1 FRXL	ferritin heavy cha
9	423	47.4	85	2 S68315	ferritin H chain -
10	423	47.4	176	2 A27805	ferritin chain H -
11	419	46.9	176	1 FRGL	ferritin, tadpole
12	403.5	45.2	176	2 C27805	ferritin chain M -
13	401	44.9	174	2 B27805	ferritin chain L -
14	386	43.2	170	2 T33854	hypothetical prote
15	372	41.7	173	1 B45628	ferritin heavy cha
16	348	39.0	170	2 T31870	hypothetical prote
17	346	38.7	175	2 S01239	ferritin light cha
18	341	38.2	175	2 JC7238	ferritin protein l
19	341	38.2	183	1 FRFL	ferritin light cha
20	339	38.0	183	2 I54774	ferritin light cha
21	328.5	36.8	181	2 S62651	ferritin - signal
22	321	35.9	183	2 B3355	ferritin light cha
23	320	35.8	175	1 FRHL	ferritin light cha
24	316	35.4	175	1 FRHL	ferritin light cha
25	303	33.9	250	2 A40992	ferritin precursor
26	297.5	33.3	254	2 T08593	ferritin precursor
27	289	32.4	250	2 T08124	ferritin 2 precurs
28	288	32.3	254	1 FRFB	ferritin heavy cha
29	287	32.1	259	2 G84827	probable ferritin

30	283	31.7	256	2 T08123	ferritin 3 precurs
31	282	31.6	285	2 S22498	ferritin precursor
32	281	31.5	253	2 S27358	ferritin precursor
33	280	31.4	300	2 S24057	ferritin 2 precurs
34	273.5	30.6	255	2 S71880	ferritin 1 precurs
35	268	30.0	172	1 A45628	ferritin heavy cha
36	266	29.8	259	2 T47726	hypothetical prote
37	187.5	21.0	239	2 S45604	ferritin precursor
38	186.5	20.9	173	2 B63354	ferritin homolog -
39	183	20.5	164	2 E72293	ferritin - Thermot
40	180.5	20.2	171	2 G69077	ferritin like prot
41	155	17.4	31	2 S04980	ferritin heavy cha
42	150	16.8	72	2 P06113	ferritin 5 - cowpe
43	145	16.2	49	2 S68314	ferritin L chain -
44	144	16.1	169	2 D83790	ferritin BH1124 [1
45	143	16.0	72	2 P06615	ferritin 1 - cowpe

#### ALIGNMENTS

#### RESULT 1

FRHUH

ferritin heavy chain - human

N:Alternate names: apoferritin H; ferritin heavy polypeptide 1

C:Species: Homo sapiens (man)

C>Date: 28-Aug-1985 #sequence revision 31-Dec-1993 #text change 09-Jul-2004

C:Accession: A23517; A25045; J2920; A24844; A03269; A05250; P05562

R:Costanzo, F.; Colombo, M.; Staempfli, S.; Santoro, C.; Marone, M.; Frank, R.; Delius,

Nucleic Acids Res. 14, 721-736, 1986

A>Title: Structure of gene and pseudogenes of human apoferritin H.

A:Reference number: A25045; MUID:86120367; PMID:3003694

A:Accession: A23517

A:Molecule type: DNA

A:Residues: 1-183 <COS>

A:Cross-references: UNIPROT:P02794; GB:X03487; NID:G31340; PIDN:CAA27205.1; PID:G762940,

R:Hentze, M.W.; Keim, S.; Papadopoulos, P.; O'Brien, S.; Modi, W.; Drysdale, J.; Leonar,

Proc. Natl. Acad. Sci. U.S.A. 83, 7226-7230, 1986

A>Title: Cloning, characterization, expression, and chromosomal localization of a human

A:Reference number: A25045; MUID:87016920; PMID:3020541

A:Accession: A25045

A:Molecule type: DNA

A:Residues: 1-183 <HEN>

A:Cross-references: GB:M14211; GB:M14212; NID:G182509; PIDN:AAA52438.1; PID:G182511; GB

R:Dhar, M.; Chauthaiwale, V.; Joshi, J.G.

Gene 126, 275-278, 1993

A>Title: Sequence of a cDNA encoding the ferritin H-chain from an 11-week-old human fet-

A:Reference number: JN0571; MUID:93246257; PMID:7916709

A:Accession: JN0571

A:Molecule type: mRNA

A:Residues: 1-183 <DHA>

A:Cross-references: GB:M97164; NID:G306743; PIDN:AAA35832.1; PID:G306744

R:Boyd, D.; Vecoli, C.; Belcher, D.M.; Jain, S.K.; Drysdale, J.W.

J. Biol. Chem. 260, 11755-11761, 1985

A>Title: Structural and functional relationships of human ferritin H and L chains deduc-

A:Reference number: A92494; MUID:86008223; PMID:3840162

A:Accession: A23920

A:Molecule type: mRNA

A:Residues: 1-183 <BOY>

A:Cross-references: GB:M11146; NID:G182504; PIDN:AAA52437.1; PID:G182505

R:Chou, C.C.; Gatti, R.A.; Fuller, M.L.; Concannon, P.; Wong, A.; Chada, S.; Davis, R.C

Mol. Cell. Biol. 6, 566-573, 1986

A>Title: Structure and expression of ferritin genes in a human promyelocytic cell line

A:Reference number: A93087; MUID:87064341; PMID:3023856

A:Accession: A24844

A:Molecule type: mRNA

A:Residues: 1-183 <CHO>

A:Cross-references: GB:M12937; NID:G182506; PIDN:AAA35830.1; PID:G182507

A>Note: the authors translated the codon CAG for residue 113 as Glu

R:Costanzo, F.; Santoro, C.; Colantuoni, V.; Bensi, G.; Raugel, G.; Romano, V.; Cortese,

EMBO J. 3, 23-27, 1984

A>Title: Cloning and sequencing of a full length cDNA coding for a human apoferritin H

A:Reference number: A03269; MUID:84158535; PMID:6323167



```
Db 1 MTTASPSQVRQNYHQDAEAAINRQINLELYASYVYLSMSCYFDRDDVALKNFAKYFLHQS 60
Qy 61 HEERHAEKLMKLNQGRGRIPLQDIKKPCDDWESGLNAMECALHLEKNVNSQLLEPPS 120
Db 61 HEERHAEKLMKLNQGRGRIPLQDIKKPCDDWESGLNAMECALHLEKSVNQSLLEL-- 118
Qy 121 PISPSPSCWHYTTNRPOQHHL 143
Db 119 -----HKLATDKNDP--HL 130

RESULT 4
ferritin heavy chain - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 09-Jul-2004
C:Accession: A39884; A05251; A15903; I52222
R:Murray, M.T.; White, K.; Munro, H.N.
Proc. Natl. Acad. Sci. U.S.A. 84, 7438-7442, 1987
A:Title: Conservation of ferritin heavy subunit gene structure: implications for the reg
A:Reference number: A39884; MUID:88041121; PMID:3478702
A:Accession: A39884
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-181 <MUR>
A:CROSS-references: UNIPROT:P19132; GB:M18053; NID:G204126; PIDN:AAA41153.1; PID:G204128
R:Leibold, E.A.; Aziz, N.; Brown, A.J.P.; Munro, H.N.
J. Biol. Chem. 259, 4327-4334, 1984
A:Title: Conservation in rat liver of light and heavy subunit sequences of mammalian fer
A:Reference number: A92474; MUID:84162134; PMID:6546756
A:Accession: A05251
A:Molecule type: protein
A:Residues: 158-180, E' <LEI>
A:Experimental source: liver
R:Huberman, A.; Barahona, E.
Biochim. Biophys. Acta 533, 51-56, 1978
A:Title: Primary structure of rat liver apoferritin. The amino end.
A:Reference number: A15903; MUID:78144897; PMID:638195
A:Accession: A15903
A:Molecule type: protein
A:Residues: 4,6-7 <HUB>
R:Ursini, M.V.; de Franciscis, V.
Biochem. Biophys. Res. Commun. 150, 287-295, 1988
A:Title: TSH regulation of ferritin H chain messenger RNA levels in the rat thyroids.
A:Reference number: I52222; MUID:88106597; PMID:2827671
A:Accession: I52222
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 136-181 <RES>
A:CROSS-references: GB:M29330; NID:G207527; PIDN:AAA42300.1; PID:G207528
C:Superfamily: ferritin
C:Keywords: acetylated amino end; iron storage
P:4/Modified site: acetylated amino end (Ser) (in mature form) #status experimental

Query Match 64.2%; Score 573.5; DB 2; Length 181;
Best Local Similarity 81.0%; Pred. No. 1.3e-45;
Matches 115; Conservative 4; Mismatches 10; Indels 13; Gaps 2;

Qy 2 TTASTSQVRQNYHQDSEAINRQINLELYASYVYLSMSCYFDRDDVALKNFAKYFLHOSH 61
Db 1 TTASTSQVRQNYHQDSEAINRQINLELYASYVYLSMSCYFDRDDVALKNFAKYFLHOSH 60
Qy 62 EERHAEKLMKLNQGRGRIPLQDIKKPCDDWESGLNAMECALHLEKNVNSQLLEPPSP 121
Db 61 EERHAEKLMKLNQGRGRIPLQDIKKPCDDWESGLNAMECALHLEKSVNQSLLEL--- 117
Qy 122 ISPPSPSCWHYTTNRPOQHHL 143
Db 118 -----HKLATDKNDP--HL 129

RESULT 5
ferritin heavy chain - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 09-Jul-2004
C:Accession: A39884; A05251; A15903; I52222
R:Murray, M.T.; White, K.; Munro, H.N.
Proc. Natl. Acad. Sci. U.S.A. 84, 7438-7442, 1987
A:Title: Conservation of ferritin heavy subunit gene structure: implications for the reg
A:Reference number: A39884; MUID:88041121; PMID:3478702
A:Accession: A39884
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-181 <MUR>
A:CROSS-references: UNIPROT:P19132; GB:M18053; NID:G204126; PIDN:AAA41153.1; PID:G204128
R:Leibold, E.A.; Aziz, N.; Brown, A.J.P.; Munro, H.N.
J. Biol. Chem. 259, 4327-4334, 1984
A:Title: Conservation in rat liver of light and heavy subunit sequences of mammalian fer
A:Reference number: A92474; MUID:84162134; PMID:6546756
A:Accession: A05251
A:Molecule type: protein
A:Residues: 158-180, E' <LEI>
A:Experimental source: liver
R:Huberman, A.; Barahona, E.
Biochim. Biophys. Acta 533, 51-56, 1978
A:Title: Primary structure of rat liver apoferritin. The amino end.
A:Reference number: A15903; MUID:78144897; PMID:638195
A:Accession: A15903
A:Molecule type: protein
A:Residues: 4,6-7 <HUB>
R:Ursini, M.V.; de Franciscis, V.
Biochem. Biophys. Res. Commun. 150, 287-295, 1988
A:Title: TSH regulation of ferritin H chain messenger RNA levels in the rat thyroids.
A:Reference number: I52222; MUID:88106597; PMID:2827671
A:Accession: I52222
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 136-181 <RES>
A:CROSS-references: GB:M29330; NID:G207527; PIDN:AAA42300.1; PID:G207528
C:Superfamily: ferritin
C:Keywords: acetylated amino end; iron storage
P:4/Modified site: acetylated amino end (Ser) (in mature form) #status experimental

Query Match 64.2%; Score 573.5; DB 2; Length 181;
Best Local Similarity 81.0%; Pred. No. 1.3e-45;
Matches 115; Conservative 4; Mismatches 10; Indels 13; Gaps 2;

Qy 2 TTASTSQVRQNYHQDSEAINRQINLELYASYVYLSMSCYFDRDDVALKNFAKYFLHOSH 61
Db 1 TTASTSQVRQNYHQDSEAINRQINLELYASYVYLSMSCYFDRDDVALKNFAKYFLHOSH 60
Qy 62 EERHAEKLMKLNQGRGRIPLQDIKKPCDDWESGLNAMECALHLEKNVNSQLLEPPSP 121
Db 61 EERHAEKLMKLNQGRGRIPLQDIKKPCDDWESGLNAMECALHLEKSVNQSLLEL--- 117
Qy 122 ISPPSPSCWHYTTNRPOQHHL 143
Db 118 -----HKLATDKNDP--HL 129
```

```
A26886
ferritin heavy chain - chicken
C:Species: Gallus gallus (chicken)
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C:Accession: A26886
R:Stevens, P.W.; Dodgson, J.B.; Engel, J.D.
Mol. Cell. Biol. 7, 1751-1758, 1987
A:Title: Structure and expression of the chicken ferritin H-subunit gene.
A:Reference number: A26886; MUID:87257874; PMID:3606643
A:Accession: A26886
A:Molecule type: DNA
A:Residues: 1-180 <STE>
A:CROSS-references: UNIPROT:P08267; GB:M16343; NID:G211773; PIDN:AAA48768.1; PID:G211774
C:Genetics:
A:Introns: 37/3; 86/3; 128/3
C:Superfamily: ferritin

Query Match 62.8%; Score 560.5; DB 2; Length 180;
Best Local Similarity 81.0%; Pred. No. 2e-44;
Matches 111; Conservative 3; Mismatches 10; Indels 13; Gaps 2;

Qy 7 SQVRQNYHQDSEAINRQINLELYASYVYLSMSCYFDRDDVALKNFAKYFLHQSHEERH 66
Db 6 SQVRQNYHQDSEAINRQINLELYASYVYLSMSCYFDRDDVALKNFAKYFLHQSHEERH 65
Qy 67 AEKLMKLNQGRGRIPLQDIKKPCDDWESGLNAMECALHLEKNVNSQLLEPPSPISPS 126
Db 66 AEKLMKLNQGRGRIPLQDIKKPCDDWESGLNAMECALHLEKNVNSQLLEP----- 117
Qy 127 SCWHYTTNRPOQHHL 143
Db 118 ---HKLATDKNDP--HL 129

RESULT 6
I46710
ferritin heavy chain - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C:Accession: I46710
R:Liau, G.; Chan, L.M.; Feng, P.
J. Biol. Chem. 266, 18819-18826, 1991
A:Title: Increased ferritin gene expression is both promoted by cAMP and a marker of gr
A:Reference number: I46677; MUID:92011647; PMID:1655764
A:Accession: I46710
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-164 <LIA>
A:CROSS-references: UNIPROT:P25915; GB:M63912; NID:G165012; PIDN:AAA31247.1; PID:G16501
C:Superfamily: ferritin

Query Match 55.9%; Score 499.5; DB 2; Length 164;
Best Local Similarity 79.8%; Pred. No. 7.4e-39;
Matches 99; Conservative 5; Mismatches 7; Indels 13; Gaps 2;

Qy 20 AINRQINLELYASYVYLSMSCYFDRDDVALKNFAKYFLHQSHEERHQAELKLNQORGG 79
Db 1 AINRQINLELYASYVYLSMSCYFDRDDVALKNFAKYFLHQSHEERHQAELKLNQORGG 60
Qy 80 RIFLQDIKKPCDDWESGLNAMECALHLEKNVNSQLLEPPSPISPSPCWHYTTNRPOP 139
Db 61 RIFLQDIKKPCDDWESGLNAMECALHLEKNVNSQLLEP-----HKLATDKNDP 109
Qy 140 QHHL 143
Db 110 ---HL 111

RESULT 7
S45603
ferritin, soma - great pond snail
C:Species: Lymnaea stagnalis (great pond snail)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
```

C;Accession: S45603; S31358  
 R;von Darl, M.; Harrison, P.M.; Bottke, W.  
 Eur. J. Biochem. 222, 353-366, 1994  
 A;Title: cDNA cloning and deduced amino acid sequence of two ferritins: soma ferritin and  
 A;Reference number: S45603; MUID:94291629; PMID:7517354  
 A;Accession: S45603  
 A;Molecule type: mRNA  
 A;Residues: 1-174 <VON>  
 A;Cross-references: UNIPROT:P42577; EMBL:X56778; NID:g9649; PIDN:CAA40096.1; PID:g9650  
 A;Experimental source: adult; visceral mass  
 A;Note: in the authors' translation 134-Glu is not shown, residues 135-141 are displaced  
 C;Complex: functional molecule is composed of 24 chains  
 C;Function:  
 A;Description: intracellular protein that stores and transports iron in a soluble, nontoxic  
 C;Superfamily: ferritin  
 C;Keywords: iron; iron binding; iron storage; iron transport; metalloprotein  
 F;25,59,60,62,63,105/Binding site: iron (Glu, Glu, Glu, His, Glu) #status predicted  
 F;82/Binding site: iron (Asp) (shared with tetrameric partners) #status predicted  
 F;84/Binding site: iron (Lys) (shared with tetrameric partners) #status predicted

Query Match 49.2%; Score 439; DB 2; Length 174;  
 Best Local Similarity 74.3%; Pred. No. 3e-33;  
 Matches 84; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

Qy 5 STSQVRQNYHQDSEAINRQINLELYASYVLSMSYFFDRDDVALKNFAKFLHQSHEER 64  
 Db 2 SVSQARQNYHAESEAGINRQINMELYASYQSMAYFFDRDDVALPGPHKFFKHQSEER 61

Qy 65 QHAEKLMKLNQGRIFLODIKKDDCDWESGLNAMECALHLEKNVQSLLE 117  
 Db 62 EHAELMKYQNKGRGRIVLQDIKKPDRDEWGTGLEAMQVALQLEKSVNQSLLD 114

RESULT 8  
 FXKL  
 ferritin heavy chain - African clawed frog  
 C;Species: Xenopus laevis (African clawed frog)  
 C;Date: 30-Sep-1991 #sequence revision 03-Nov-1995 #text\_change 09-Jul-2004  
 C;Accession: A37959; S12463; S09499; A40408  
 R;Holland, L.J.; Wall, A.A.; Bhattacharya, A.  
 Biochemistry 30, 1965-1972, 1991  
 A;Title: Xenopus liver ferritin H subunit: cDNA sequence and mRNA production in the liver  
 A;Reference number: A37959; MUID:91129281; PMID:1993207  
 A;Accession: A37959  
 A;Molecule type: mRNA  
 A;Residues: 1-176 <HOL>  
 A;Cross-references: UNIPROT:P17663; GB:M55010; NID:g214135; PIDN:AAA49708.1; PID:g214136  
 A;Experimental source: liver  
 R;Schoenberg, D.  
 submitted to the EMBL Data Library, January 1990  
 A;Reference number: S12463  
 A;Accession: S12463  
 A;Molecule type: mRNA  
 A;Residues: 1-5, 'L', 7-14, 'I', 16-156, 'A', 159-176 <SCH>  
 A;Cross-references: EMBL:X51395; NID:g64690; PIDN:CAA35760.1; PID:g64691  
 R;Moskaitis, J.E.; Pastori, R.L.; Schoenberg, D.R.  
 Nucleic Acids Res. 18, 2184, 1990  
 A;Title: Sequence of Xenopus laevis ferritin mRNA.  
 A;Reference number: S09499; MUID:90245677; PMID:2336402  
 A;Accession: S09499  
 A;Molecule type: mRNA  
 A;Residues: 1-5, 'L', 7-14, 'I', 16-64, 70-86, 'KFLKY', 87-156, 'A', 159-176 <MOS>  
 A;Cross-references: EMBL:X51395  
 A;Note: the sequence shown in the alignment is inconsistent with the nucleotide sequence  
 R;Muller, J.P.; Vedel, M.; Monnot, M.J.; Tourzet, N.; Wegner, M.  
 DNA Cell Biol. 10, 571-579, 1991  
 A;Title: Molecular cloning and expression of ferritin mRNA in heavy metal-poisoned Xenopus  
 A;Reference number: A40408; MUID:92029619; PMID:1718317  
 A;Accession: A40408  
 A;Molecule type: mRNA  
 A;Residues: 1-9, 'H', 11-22, 'W', 24-90, 'G', 92-96, 'T', 98-123, 'AH', 126-143, 'Q', 145-176 <MUL>  
 A;Cross-references: EMBL:X64727  
 A;Experimental source: cadmium-poisoned XL2 embryonic cell line

C;Complex: The functional molecule is composed of 24 chains, is roughly spherical and co  
 C;Function:  
 A;Description: intracellular protein that stores and transports iron in a soluble, nontoxic  
 C;Superfamily: ferritin  
 C;Keywords: iron; iron binding; iron storage; iron transport; metalloprotein; multimer  
 F;24,58,59,61,62,104/Binding site: iron (Glu, Glu, Glu, His, Glu) #status predicted  
 F;81/Binding site: iron (Asp) (shared with tetrameric partners) #status predicted  
 F;83/Binding site: iron (Lys) (shared with tetrameric partners) #status predicted

Query Match 47.5%; Score 424.5; DB 1; Length 176;  
 Best Local Similarity 60.4%; Pred. No. 6.5e-32;  
 Matches 81; Conservative 19; Mismatches 23; Indels 11; Gaps 1;

Qy 7 SQVRQNYHQDSEAINRQINLELYASYVLSMSYFFDRDDVALKNFAKFLHQSHEERQH 66  
 Db 3 SQVRQNFNSDCEAINRQINMELYASYVLSMSYFFDRDDVALHVAKFFKEQSHREH 62

Qy 67 AEKLMKLNQGRGRIFLODIKKDDCDWESGLNAMECALHLEKNVQSLLEFPSPISPS 126  
 Db 63 AEKFLKYQNKGRGRVWLQDIKKPDERDEWSNLEAMQALQLEKTVNQALLDL----- 114

Qy 127 SCWHHYTTNRPPQ 140  
 Db 115 ---HKLASDKVDPQ 125

RESULT 9  
 S68315  
 ferritin H chain - guinea pig (fragment)  
 C;Species: Cavia porcellus (guinea pig)  
 C;Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 20-Aug-1999  
 C;Accession: S68315  
 R;Gosiewska, A.; Mahmoodian, F.; Peterkofsky, B.  
 Arch. Biochem. Biophys. 325, 295-303, 1996  
 A;Title: Gene expression of iron-related proteins during iron deficiency caused by scur  
 A;Reference number: S68313; MUID:96139112; PMID:8561510  
 A;Accession: S68315  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-85 <GOS>  
 A;Cross-references: GB:S91307; NID:g1336695; PIDN:AAB35970.1; PID:g1336696  
 C;Superfamily: ferritin

Query Match 47.4%; Score 423; DB 2; Length 85;  
 Best Local Similarity 94.1%; Pred. No. 3.7e-32;  
 Matches 80; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 31 ASYVLSMSYFFDRDDVALKNFAKFLHQSHEERQHAELMKLNQGRGRIFLODIKKPD 90  
 Db 1 ASYVLSMSYFFDRDDVALKNFAKFLHQSHEERQHAELMKLNQGRGRIFLODIKKPD 60

Qy 91 CDDWESGLNAMECALHLEKNVQSL 115  
 Db 61 RDDWENGLNAMECALHLEKSVNQSL 85

RESULT 10  
 A27805  
 ferritin chain H - bullfrog  
 C;Species: Rana catesbeiana (bullfrog)  
 C;Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 09-Jul-2004  
 C;Accession: A27805  
 R;Dickey, L.F.; Sreedharan, S.; Theil, E.C.; Didsbury, J.R.; Wang, Y.H.; Kaufman, R.E.  
 J. Biol. Chem. 262, 7901-7907, 1987  
 A;Title: Differences in the regulation of messenger RNA for housekeeping and specialized  
 ntification of the first processed pseudogene in amphibia.  
 A;Reference number: A92648; MUID:87222424; PMID:3495534  
 A;Accession: A27805  
 A;Molecule type: mRNA  
 A;Residues: 1-176 <DIC>  
 A;Cross-references: UNIPROT:P07229; GB:M15655; NID:g213672; PIDN:AAA49523.1; PID:g213673  
 C;Superfamily: ferritin

Query Match 47.4%; Score 423; DB 2; Length 176;  
Best Local Similarity 70.3%; Pred. No. 9e-32;  
Matches 78; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

QY 7 SQVRQNYHDSAAINRQINLELYASYVLSMSYFFDRDDVALKNFAKYFLHQSHEERQH 66  
DB 3 SQVRQNYHDSAAINRQINLELYASYVLSMAFYFDRDDIALHNVAKFFKEQSHEERH 62

QY 67 AEKLMKLNQGRGRIFFLODIKKPCDDWESGLNAMECALHLEKNVQSILLE 117  
DB 63 AEKLMKLNQGRGRIFFLODIKKPCDDWESGLNAMECALHLEKNVQSILLE 113

RESULT 11  
ferritin, tadpole - bullfrog  
C:Species: Rana catesbeiana (bullfrog)  
C>Date: 31-Mar-1988 #sequence\_revision 31-Mar-1988 #text\_change 09-Jul-2004  
C:Accession: A25627  
R:Dickey, J.R.; Theil, E.C.; Kaufman, R.E.; Dickey, L.F.  
J. Biol. Chem. 261, 949-955, 1986  
A:Title: Multiple red cell ferritin mRNAs, which code for an abundant protein in the embryo  
A:Reference number: A25627; MUID:86085940; PMID:3484480  
A:Accession: A25627  
A:Molecule type: mRNA  
A:Residues: 1-176 <DID>  
A:Cross-references: UNIPROT:P07229; GB:M12120; NID:G213691; PIDN:AAA49532.1; PID:G213692  
A:Experimental source: reticulocytes  
C:Comment: The sequence of this ferritin is more similar to mammalian H chains than to I  
C:Superfamily: ferritin  
C:Keywords: erythrocyte; iron storage

Query Match 46.9%; Score 419; DB 1; Length 176;  
Best Local Similarity 69.4%; Pred. No. 2.1e-31;  
Matches 77; Conservative 18; Mismatches 16; Indels 0; Gaps 0;

QY 7 SQVRQNYHDSAAINRQINLELYASYVLSMSYFFDRDDVALKNFAKYFLHQSHEERQH 66  
DB 3 SQVRQNYHDSAAINRQINLELYASYVLSMAFYFDRDDIALHNVAKFFKEQSHEERH 62

QY 67 AEKLMKLNQGRGRIFFLODIKKPCDDWESGLNAMECALHLEKNVQSILLE 117  
DB 63 AEKLMKLNQGRGRIFFLODIKKPCDDWESGLNAMECALHLEKNVQSILLE 113

RESULT 12  
ferritin chain M - bullfrog  
C:Species: Rana catesbeiana (bullfrog)  
C>Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 09-Jul-2004  
C:Accession: C27805  
R:Dickey, L.F.; Sreedharan, S.; Theil, E.C.; Didsbury, J.R.; Wang, Y.H.; Kaufman, R.E.  
J. Biol. Chem. 262, 7901-7907, 1987  
A:Title: Differences in the regulation of messenger RNA for housekeeping and specialized  
n-tification of the first processed pseudogene in amphibia.  
A:Reference number: A32648; MUID:87222424; PMID:3495534  
A:Accession: C27805  
A:Molecule type: mRNA  
A:Residues: 1-176 <DIC>  
A:Cross-references: UNIPROT:P07798; GB:J02724; NID:G213676; PIDN:AAA49525.1; PID:G213677  
C:Superfamily: ferritin

Query Match 45.2%; Score 403.5; DB 2; Length 176;  
Best Local Similarity 58.4%; Pred. No. 5.6e-30;  
Matches 80; Conservative 16; Mismatches 28; Indels 13; Gaps 2;

QY 7 SQVRQNYHDSAAINRQINLELYASYVLSMSYFFDRDDVALKNFAKYFLHQSHEERQH 66  
DB 3 SQVRQNYHDSAAINRQINLELYASYVLSMAFYFDRDDIALHNVAKFFKEQSHEERH 62

QY 67 AEKLMKLNQGRGRIFFLODIKKPCDDWESGLNAMECALHLEKNVQSILLEPSPSP 126  
DB 63 AEKLMKLNQGRGRIFFLODIKKPCDDWESGLNAMECALHLEKNVQSILLEPSPSP 114

QY 127 SCWHYTTNRQPQHLL 143  
DB 115 ---HKLATDKVDP--HL 126

RESULT 13  
ferritin chain L - bullfrog  
C:Species: Rana catesbeiana (bullfrog)  
C>Date: 16-Aug-1988 #sequence\_revision 31-Dec-1988 #text\_change 18-Jun-1993  
C:Accession: B27805  
R:Dickey, L.F.; Sreedharan, S.; Theil, E.C.; Didsbury, J.R.; Wang, Y.H.; Kaufman, R.E.  
J. Biol. Chem. 262, 7901-7907, 1987  
A:Title: Differences in the regulation of messenger RNA for housekeeping and specialized  
n-tification of the first processed pseudogene in amphibia.  
A:Reference number: A32648; MUID:87222424; PMID:3495534  
A:Accession: B27805  
A:Molecule type: mRNA  
A:Residues: 1-174 <DIC>  
C:Superfamily: ferritin

Query Match 44.9%; Score 401; DB 2; Length 174;  
Best Local Similarity 64.0%; Pred. No. 9.4e-30;  
Matches 71; Conservative 25; Mismatches 15; Indels 0; Gaps 0;

QY 7 SQVRQNYHDSAAINRQINLELYASYVLSMSYFFDRDDVALKNFAKYFLHQSHEERQH 66  
DB 3 SQVRQNYHDSAAINRQINLELYASYVLSMAFYFDRDDIALHNVAKFFKEQSHEERH 62

QY 67 AEKLMKLNQGRGRIFFLODIKKPCDDWESGLNAMECALHLEKNVQSILLE 117  
DB 63 AEKLMKLNQGRGRIFFLODIKKPCDDWESGLNAMECALHLEKNVQSILLE 113

RESULT 14  
T33854  
hypotheical protein D1037.3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T33854  
R:Ledwith, J.; Biewald, T.  
submitted to the EMBL Data Library, November 1998  
A:Description: The sequence of C. elegans cosmid D1037.  
A:Reference number: Z21424  
A:Accession: T33854  
A>Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-170 <LED>  
A:Cross-references: UNIPROT:Q9TYS3; EMBL:AF106592; PIDN:AAC78491.1; GSPDB:GNO0019; CESP  
A:Experimental source: strain Bristol N2; clone D1037  
C:Genetics:  
A:Gene: CESP:D1037.3  
A:Map position: 1  
A:Introns: 19/3; 137/3  
C:Superfamily: ferritin

Query Match 43.2%; Score 386; DB 2; Length 170;  
Best Local Similarity 64.9%; Pred. No. 2.2e-28;  
Matches 74; Conservative 17; Mismatches 23; Indels 0; Gaps 0;

QY 7 SQVRQNYHDSAAINRQINLELYASYVLSMSYFFDRDDVALKNFAKYFLHQSHEERQH 66  
DB 2 SLARQNYHSVEAAVKNQINLELYASYVLSMSYFFDRDDVALPNIAKFFKEQSDEEREH 61

QY 67 AEKLMKLNQGRGRIFFLODIKKPCDDWESGLNAMECALHLEKNVQSILLEPSPS 120  
DB 62 ATELMLRQNLGRGVLDIQRKPEDEWGTALKAFAALALEKFNESLULKHS 115

RESULT 15  
B45628  
ferritin heavy chain 1 - fluke (Schistosoma mansoni)

C:Species: Schistosoma mansoni  
C:Date: 22-Apr-1993 #sequence\_revision 02-Jun-1994 #text\_change 09-Jul-2004  
C:Accession: B45628  
R:Dietzel, J.; Hirzmann, J.; Preis, D.; Symmons, P.; Kunz, W.  
Mol. Biochem. Parasitol. 50, 245-254, 1992  
A:Title: Ferritins of Schistosoma mansoni: sequence comparison and expression in female  
A:Reference number: A45628; MUID:92158004; PMID:1741011  
A:Accession: B45628  
A:Molecule type: mRNA  
A:Residues: 1-173 <DIE>  
A:Cross-references: UNIPROT:P25319; GB:M64538; NID:g160985; PIDN:AA29880.1; PID:g160986  
A>Note: sequence extracted from NCBI backbone (NCBIN:82751, NCBIIP:82752)  
C:Superfamily: ferritin  
C:Keywords: iron; iron storage; metalloprotein  
F:23,57,58,60,61,103/Binding site: iron (Glu, Glu, Glu, His, Glu) #status predicted

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Query Match	41.7%	Score 372;	DB 1;	Length 173;
Best Local Similarity	64.0%	Pred. No. 4.4e-27;		
Matches 71;	Conservative 17;	Mismatches 23;	Indels 0;	Gaps 0;

  

QY	7	SOVQNYHQDSEAAINRQINLELYASYVYLSMSYYFDRDDVALKNFAKYFLHQSHHEERQH	66
Db	2	SLCRQNYHEECBAGVYKQINMELYASYVYMTWAFHNRDDVALNGFYKFFLNSESEERQH	61

  

QY	67	AEKLMKLNQGRGRIFLODIKKPDCDDWESGLNAMECALHLEKNVNSLLE	117
Db	62	AIKLMTYQNMRGRIVLQDISAPQLSWNSGLHMQDALDLEKKVNSLME	112

Search completed: March 30, 2005, 19:42:58  
Job time : 17 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 30, 2005, 19:37:59 ; Search time 52 Seconds  
(without alignments)  
1050.609 Million cell updates/sec

Title: US-09-786-867C-5

Perfect score: 893

Sequence: 1 MTTASTQVRQNYHQDSEAA.....PRRRKRPHSIPTLIRSP 165

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

1:	/cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2:	/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3:	/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4:	/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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7:	/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
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16:	/cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17:	/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18:	/cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19:	/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20:	/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	615.5	68.9	183	15	US-10-384-496-2
2	615.5	68.9	183	17	US-10-734-049A-231
3	615.5	68.9	190	15	US-10-435-666-8
4	615.5	68.9	190	16	US-10-734-564-127
5	583.5	65.3	182	15	US-10-384-496-12
6	583.5	65.0	182	15	US-10-384-496-6
7	579.5	64.9	180	14	US-10-324-153-4
8	523.5	58.6	127	15	US-10-264-049-3406
9	494	55.3	242	14	US-10-324-153-2
10	477	53.4	173	15	US-10-216-464-29
11	400.5	44.8	121	15	US-10-042-865-176
12	399	44.7	183	9	US-09-801-574-70
13	390.5	43.7	183	15	US-10-092-900A-260

14	387.5	43.4	204	16	US-10-478-758-9	Sequence 9, Appli
15	379.5	42.5	178	14	US-10-029-386-32858	Sequence 32858, A
16	375.5	42.0	221	9	US-09-801-574-68	Sequence 68, Appli
17	361	40.4	85	9	US-09-925-302-812	Sequence 812, App
18	361	40.4	85	10	US-09-925-302-812	Sequence 812, App
19	343	38.4	199	16	US-10-363-829-400	Sequence 400, App
20	341	38.2	183	15	US-10-384-496-14	Sequence 14, Appli
21	338	37.8	175	15	US-10-042-865-172	Sequence 172, App
22	338	37.8	183	15	US-10-384-496-10	Sequence 10, Appli
23	338	37.8	183	15	US-10-042-865-175	Sequence 175, App
24	335	37.5	183	15	US-10-042-865-173	Sequence 173, App
25	325.5	36.5	175	15	US-10-042-865-171	Sequence 171, App
26	321	35.9	183	15	US-10-384-496-8	Sequence 8, Appli
27	320	35.8	175	15	US-10-042-865-174	Sequence 174, App
28	316	35.4	175	10	US-09-919-039-333	Sequence 333, App
29	316	35.4	175	15	US-10-435-666-4	Sequence 4, Appli
30	316	35.4	175	15	US-10-262-445-56	Sequence 56, Appli
31	316	35.4	175	16	US-10-734-564-128	Sequence 128, App
32	316	35.4	254	15	US-10-104-047-3198	Sequence 3198, Ap
33	315	35.3	176	9	US-09-801-574-28	Sequence 28, Appli
34	312	34.9	154	14	US-10-029-386-29603	Sequence 29603, A
35	303	33.9	250	15	US-10-424-599-184909	Sequence 184909,
36	298	33.4	262	15	US-10-425-114-62139	Sequence 62139, A
37	298	33.4	262	15	US-10-425-114-63725	Sequence 63725, A
38	295	33.0	249	15	US-10-424-599-147651	Sequence 147651,
39	294	32.9	250	9	US-09-834-624-2	Sequence 2, Appli
40	294	32.9	250	9	US-09-834-624-3	Sequence 3, Appli
41	292	32.7	248	15	US-10-424-599-278212	Sequence 278212,
42	292	32.7	262	15	US-10-425-114-63721	Sequence 63721, A
43	292	32.6	262	15	US-10-425-114-63723	Sequence 63723, A
44	291	32.6	167	16	US-10-617-955-2	Sequence 2, Appli
45	291	32.6	167	16	US-10-617-955-4	Sequence 4, Appli

#### ALIGNMENTS

RESULT 1  
US-10-384-496-2  
; Sequence 2, Application US/10384496  
; Publication No. US20030219385A1  
; GENERAL INFORMATION:  
; APPLICANT: AHRENS, ERIC  
; TITLE OF INVENTION: CONTRAST AGENTS FOR MAGNETIC RESONANCE IMAGING AND  
; FILE OF INVENTION: METHODS RELATED THERETO  
; FILE REFERENCE: CMV-001.01  
; CURRENT APPLICATION NUMBER: US/10/384,496  
; CURRENT FILING DATE: 2003-03-07  
; PRIOR APPLICATION NUMBER: 60/363,163  
; PRIOR FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 183  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-384-496-2

Query Match	68.9%	Score	615.5	DB 15	Length	183			
Best Local Similarity	84.6%	Pred. No.	6.1e-55						
Matches	121	Conservative	3	Mismatches	6	Indels	13	Gaps	2
Qy	1	MTTASTQVRQNYHQDSEAA	NRQINQLLEYASYVYLSMSYFDRDDVAKNFKAYFLHQH	60					
Db	1	MTTASTQVRQNYHQDSEAA	NRQINQLLEYASYVYLSMSYFDRDDVAKNFKAYFLHQH	60					
Qy	61	HEERQHAELKMLQNGRGRI	FLODIKKPCDDWESGLNAMECALHLEKNVNSLLEPPS	120					
Db	61	HEERQHAELKMLQNGRGRI	FLODIKKPCDDWESGLNAMECALHLEKNVNSLLEPPS	118					
Qy	121	PISPSPCWHYTTNRPOQHLL	143						
Db	119	-----HKLATDKNDP--	HL 130						

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RESULT 2
US-10-734-049A-231
; Sequence 231, Application US/10734049A
; Publication No. US20050042624A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Kyogo
; APPLICANT: SHICHIGO, Shigeki
; TITLE OF INVENTION: TUMOR ANTIGEN
; FILE REFERENCE: Q-78382
; CURRENT APPLICATION NUMBER: US/10/734,049A
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/JP02/05799
; PRIOR FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: JP 2001/177058
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: JP 2001/250728
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 408
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 231
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-734-049A-231

Query Match      68.9%; Score 615.5; DB 17; Length 183;
Best Local Similarity 84.6%; Pred. No. 6.1e-55;
Matches 121; Conservative 3; Mismatches 6; Indels 13; Gaps 2;

QY 1 MTTASTSOVRQNYHODSEAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHQS 60
Db 1 MTTASTSOVRQNYHODSEAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHQS 60
QY 61 HEERQHAELKMLQNRGGRIFLQDIKKPDCDDWESGLNAMECALHLEKNVNSLLEP 120
Db 61 HEERHAELKMLQNRGGRIFLQDIKKPDCDDWESGLNAMECALHLEKNVNSLLEP 118
QY 121 PISPPSCWHYTTNRPOQHHL 143
Db 119 -----HKLATDKNDP--HL 130

RESULT 3
US-10-435-666-8
; Sequence 8, Application US/10435666
; Publication No. US20040006001A1
; GENERAL INFORMATION:
; APPLICANT: CARTER, Daniel C.
; TITLE OF INVENTION: FERRITIN FUSION PROTEINS FOR USE IN VACCINES AND OTHER APPLICATIONS
; FILE REFERENCE: P07624W00/BAS
; CURRENT APPLICATION NUMBER: US/10/435,666
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/379,145
; PRIOR FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-435-666-8

Query Match      68.9%; Score 615.5; DB 15; Length 190;
Best Local Similarity 84.6%; Pred. No. 6.4e-55;
Matches 121; Conservative 3; Mismatches 6; Indels 13; Gaps 2;

QY 1 MTTASTSOVRQNYHODSEAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHQS 60
Db 1 MTTASTSOVRQNYHODSEAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHQS 60
QY 61 HEERQHAELKMLQNRGGRIFLQDIKKPDCDDWESGLNAMECALHLEKNVNSLLEP 120
Db 61 HEERHAELKMLQNRGGRIFLQDIKKPDCDDWESGLNAMECALHLEKNVNSLLEP 118
QY 121 PISPPSCWHYTTNRPOQHHL 143
Db 119 -----HKLATDKNDP--HL 130
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Db 61 HEERHAELKMLQNRGGRIFLQDIKKPDCDDWESGLNAMECALHLEKNVNSLLEP 118
QY 121 PISPPSCWHYTTNRPOQHHL 143
Db 119 -----HKLATDKNDP--HL 130

RESULT 4
US-10-734-564-127
; Sequence 127, Application US/10734564
; Publication No. US20040157278A1
; GENERAL INFORMATION:
; APPLICANT: Christopher C Burgess et al
; TITLE OF INVENTION: Detection Methods Using TIMP1
; FILE REFERENCE: 1657/2012
; CURRENT APPLICATION NUMBER: US/10/734,564
; CURRENT FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 127
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-734-564-127

Query Match      68.9%; Score 615.5; DB 16; Length 190;
Best Local Similarity 84.6%; Pred. No. 6.4e-55;
Matches 121; Conservative 3; Mismatches 6; Indels 13; Gaps 2;

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Db 1 MTTASTSOVRQNYHODSEAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHQS 60
QY 61 HEERQHAELKMLQNRGGRIFLQDIKKPDCDDWESGLNAMECALHLEKNVNSLLEP 120
Db 61 HEERHAELKMLQNRGGRIFLQDIKKPDCDDWESGLNAMECALHLEKNVNSLLEP 118
QY 121 PISPPSCWHYTTNRPOQHHL 143
Db 119 -----HKLATDKNDP--HL 130

RESULT 5
US-10-384-496-12
; Sequence 12, Application US/10384496
; Publication No. US20030219385A1
; GENERAL INFORMATION:
; APPLICANT: ARENS, ERIC
; TITLE OF INVENTION: CONTRAST AGENTS FOR MAGNETIC RESONANCE IMAGING AND METHODS RELATED THERETO
; FILE REFERENCE: CMV-001.01
; CURRENT APPLICATION NUMBER: US/10/384,496
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: 60/363,163
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-384-496-12

Query Match      65.3%; Score 583.5; DB 15; Length 182;
Best Local Similarity 81.8%; Pred. No. 1.2e-51;
Matches 117; Conservative 4; Mismatches 9; Indels 13; Gaps 2;

QY 1 MTTASTSOVRQNYHODSEAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHQS 60
Db 1 MTTASTSOVRQNYHODSEAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHQS 60
QY 61 HEERQHAELKMLQNRGGRIFLQDIKKPDCDDWESGLNAMECALHLEKNVNSLLEP 120
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Db 61 HEEREAEKMLKQNGRIFLODIKKPDRDDWESGLNAMECALHLEKSNQSLLEL-- 118  
QY 121 PISPSPCWHYTTNRPOQHLL 143  
Db 119 -----HKLATDKNDP--HL 130

## RESULT 6

US-10-384-496-6  
; Sequence 6, Application US/10384496  
; Publication No. US20030219385A1  
; GENERAL INFORMATION:  
; APPLICANT: AHRENS, ERIC  
; TITLE OF INVENTION: CONTRAST AGENTS FOR MAGNETIC RESONANCE IMAGING AND  
; TITLE OF INVENTION: METHODS RELATED THERETO  
; FILE REFERENCE: CMV-001.01  
; CURRENT APPLICATION NUMBER: US/10/384,496  
; CURRENT FILING DATE: 2003-03-07  
; PRIOR APPLICATION NUMBER: 60/363,163  
; PRIOR FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 182  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-384-496-6

Query Match 65.0%; Score 580.5; DB 15; Length 182;  
Best Local Similarity 81.1%; Pred. No. 2.4e-51;  
Matches 116; Conservative 5; Mismatches 9; Indels 13; Gaps 2;

QY 1 MTTASTSVQRNYHDSAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYFLHQS 60  
Db 1 MTTASTSVQRNYHDSAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYFLHQS 60  
QY 61 HEEREAEKMLKQNGRIFLODIKKPDRDDWESGLNAMECALHLEKSNQSLLEPFS 120  
Db 61 HEEREAEKMLKQNGRIFLODIKKPDRDDWESGLNAMECALHLEKSNQSLLEL-- 118  
QY 121 PISPSPCWHYTTNRPOQHLL 143  
Db 119 -----HKLATDKNDP--HL 130

## RESULT 7

US-10-324-153-4  
; Sequence 4, Application US/10324153  
; Publication No. US20030114645A1  
; GENERAL INFORMATION:  
; APPLICANT: LADUNGA, Steven et al  
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL000843CON  
; CURRENT APPLICATION NUMBER: US/10/324,153  
; CURRENT FILING DATE: 2002-12-20  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 180  
; TYPE: PRT  
; ORGANISM: Trichosurus vulpecula  
US-10-324-153-4

Query Match 64.9%; Score 579.5; DB 14; Length 180;  
Best Local Similarity 82.1%; Pred. No. 2.9e-51;  
Matches 115; Conservative 4; Mismatches 8; Indels 13; Gaps 2;

QY 4 ASTSVQRNYHDSAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYFLHQSHEE 63  
Db 1 SPSVQRNYHDSAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYFLHQSHEE 60

QY 64 RQHAELKMLKQNGRIFLODIKKPDRDDWESGLNAMECALHLEKSNQSLLEPSPIS 123  
Db 61 REHAELKMLKQNGRIFLODIKKPDRDDWESGLNAMECALHLEKSNQSLLEL----- 115  
QY 124 PPSPCWHYTTNRPOQHLL 143  
Db 116 -----HKLATDKNDP--HL 127

## RESULT 8

US-10-264-049-3406  
; Sequence 3406, Application US/10264049  
; Publication No. US20040005579A1  
; GENERAL INFORMATION:  
; APPLICANT: Birse et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PAJ33PI  
; CURRENT APPLICATION NUMBER: US/10/264,049  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: PCT/US01/18569  
; PRIOR FILING DATE: 2001-06-07  
; PRIOR APPLICATION NUMBER: US 60/209,467  
; PRIOR FILING DATE: 2000-06-07  
; NUMBER OF SEQ ID NOS: 4360  
; SOFTWARE: Patent In Ver. 3.1  
; SEQ ID NO 3406  
; LENGTH: 127  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-264-049-3406

Query Match 58.6%; Score 523.5; DB 15; Length 127;  
Best Local Similarity 82.4%; Pred. No. 1.1e-45;  
Matches 103; Conservative 3; Mismatches 6; Indels 13; Gaps 2;

QY 19 AAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYFLHQSHEERQHAELKMLKQNGR 78  
Db 1 AAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYFLHQSHEERQHAELKMLKQNGR 60  
QY 79 GRIFLODIKKPDRDDWESGLNAMECALHLEKSNQSLLEPSPISPCWHYTTNRQ 138  
Db 61 GRIFLODIKKPDRDDWESGLNAMECALHLEKSNQSLLEL-----HKLATDKND 109  
QY 139 POHLL 143  
Db 110 P--HL 112

## RESULT 9

US-10-324-153-2  
; Sequence 2, Application US/10324153  
; Publication No. US20030114645A1  
; GENERAL INFORMATION:  
; APPLICANT: LADUNGA, Steven et al  
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: CL000843CON  
; CURRENT APPLICATION NUMBER: US/10/324,153  
; CURRENT FILING DATE: 2002-12-20  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 242  
; TYPE: PRT  
; ORGANISM: Human  
US-10-324-153-2

Query Match 55.3%; Score 494; DB 14; Length 242;  
Best Local Similarity 83.3%; Pred. No. 2.5e-42;  
Matches 95; Conservative 9; Mismatches 10; Indels 0; Gaps 0;



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; PRIOR APPLICATION NUMBER: 60/187,518
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: 60/261,557
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-801-574-70

Query Match          44.7%; Score 399; DB 9; Length 183;
Best Local Similarity 65.0%; Pred. No. 1e-32;
Matches 76; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

QY 1 MTTASTSVQRQNHQDSAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHQS 60
Db 1 MATAQPSQVRQKYDNTCDAAINSHITLBYTSYLSMAFYFNRRDDVALENPFYFLRLS 60

QY 61 HEERQHAELKMLQNRGRIFLDIKKPCDDWESGLNAMECALHLEKNVNSLLE 117
Db 61 DDKMEHAQKMLQNLRGHICLHDIRKPCQGWESGLVAMESAPHLEKNVNSLLE 117

RESULT 13
US-10-092-900A-260
; Sequence 260, Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Miller, Charles E.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Tchernov, Velizar T.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Liu, Yi
; APPLICANT: Anderson, David W.
; APPLICANT: Spaderma, Steven K.
; APPLICANT: Catterton, Elina
; APPLICANT: Leite, Mario W.
; APPLICANT: Zhong, Hailong
; APPLICANT: Alsobrook, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-290C
; CURRENT APPLICATION NUMBER: US/10/092,900A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: USN 60/274,322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USN 60/283,675
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: USN 60/338,092
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: USN 60/274,281
; PRIOR FILING DATE: 2001-03-08
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; PRIOR APPLICATION NUMBER: USN 60/274,191
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USN 60/325,681
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: USN 60/304,354
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: USN 60/279,995
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: USN 60/294,899
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: USN 60/287,424
; PRIOR FILING DATE: 2001-04-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SEQ ID NO 260
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-900A-260

Query Match          43.7%; Score 390.5; DB 15; Length 183;
Best Local Similarity 56.7%; Pred. No. 7.4e-32;
Matches 76; Conservative 17; Mismatches 30; Indels 11; Gaps 1;

QY 7 SOVRQNHQDSAAINRQINLELYASYVYLSMSYFFDRDDVALKNFAKYFLHQSHEEROH 66
Db 7 SPVRYHHPSCAAINSHITLBYTSYLSMAFYFNRRDDVALENPFYFLRQSEKREH 66

QY 67 AEKLMKLNQNRGRIFLDIKKPCDDWESGLNAMECALHLEKNVNSLLEPPSPISPSP 126
Db 67 AQELMSLNLRGGRICLHDIRKPCQGWESGLKAMECTFHLEKNINQSLLE----- 118

QY 127 SCWHYTTNRPOQ 140
Db 119 ---HQLARENGDPQ 129

RESULT 14
US-10-478-758-9
; Sequence 9, Application US/10478758
; Publication No. US20040152874A1
; GENERAL INFORMATION:
; APPLICANT: RAUMANN, Brigitte E.
; APPLICANT: GRIFFIN, Jennifer A.
; APPLICANT: HAFALIA, April J.A.
; APPLICANT: BATRA, Sajeev
; APPLICANT: YAO, Monique G.
; APPLICANT: FORSYTHE, Ian J.
; APPLICANT: RAMKUMAR, Javalaxmi
; APPLICANT: DUGGAN, Brendan M.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: WARREN, Bridget A.
; APPLICANT: LAL, Preeti G.
; APPLICANT: GIETZEN, Kimberly J.
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: BECHA, Shanya D.
; APPLICANT: TANG, Y. Tom
; APPLICANT: YUE, Henry
; APPLICANT: CHINN, Anna M.
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PF-0980 USN
; CURRENT APPLICATION NUMBER: US/10/478,758
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: PCT/US02/16446
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/293,722
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/296,881
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/304,593
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/305,105
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; PRIOR FILING DATE: 2001-07-12
;
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PERL Program
; SEQ ID NO 9
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID
US-10-478-758-9

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Query Match	43.4%;	Score 387.5;	DB 16;	Length 204;
Best Local Similarity	55.8%;	Pred. No. 1.7e-31;		
Matches	77;	Conservative 19;	Mismatches 31;	Indels 11; Gaps 1;
Qy	3	TASTSVQRYNVHODSEAAINQINLELYASVYVLSMSYYPDRDDVALKNFAKYFLHOSHE	62	
Db	36	TAPUWQRYNVHPPCDAAVNSHVNLEHUASCYVLSMAFYLPDRDVTTLERFSRCFLSQSE	95	
Qy	63	ERQHAELKMLQNGRGRIFLQDICKPDCDDWESGLNAMECALHLEKNVQSLLEFFSP	122	
Db	96	KREHAQKLIWLQNLRGGRICLPDIWKPEREWESGLQAMECAFLERSVNYSLLEL	151	
Qy	123	SPSPSCWHYHTNRPQPO	140	
Db	152	-----HYLAWEKGDPQ	162	

RESULT 15  
US-10-029-386-32858  
; Sequence 32858, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David K.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO  
; FILE REFERENCE: AEOMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 32858  
; LENGTH: 178  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AJ239329.2  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.3  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.99  
; OTHER INFORMATION: SWISSPROT HIT: P02794, EVALUAE 4.00e-62  
US-10-029-386-32858

Query Match	42.5%	Score 379.5	DB 14	Length 178
Best Local Similarity	57.0%	Pred. No. 9.7e-31		
Matches	73	Conservative 16	Mismatches 28	Indels 11
				Gaps 1
Qy	13	YH05EAAINRQINLEIYASYVYLSMGSYFDRDDVALKNFAKYFLHOSHSEERQHAELMK	72	
Db	2	HHFSCAAINTHISLELHASVYLSMAFYFDODDALEHFDYFLRQSQEKREHAQELMS	61	
Qy	73	LQNRGGRIFLQDIKKPDCDDWESGLNABECALHLEKNVNSQLLEFPSPSPSCWHHY	132	
Db	62	LQNLRRGRICLHDIRKEPGQGWESGLKAMECTPHLEKNINQSLLEL	110	
Qy	133	TTNRPPQO	140	

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OM protein - protein search, using sw model

Run on: March 30, 2005, 19:34:31 ; Search time 22 Seconds  
(without alignments)  
559.868 Million cell updates/sec

Title: US-09-786-867C-5  
Perfect score: 893  
Sequence: 1 MTTASTQVRQNYHQDSEAA.....PRRKRPHSIPTILIRSP 165

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2\_6/ptodata/1/iaa/6B COMB.pap:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pap:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	615.5	68.9	220	4	US-09-949-016-10773 Sequence 10773, A
2	316	35.4	175	4	US-09-919-039-333 Sequence 333, App
3	312	34.9	238	4	US-09-949-016-10295 Sequence 10295, A
4	294	32.9	250	4	US-09-418-830-2 Sequence 2, Appli
5	294	32.9	250	4	US-09-418-830-3 Sequence 3, Appli
6	293.5	32.9	107	4	US-09-621-976-4402 Sequence 4402, Ap
7	177	19.8	243	2	US-08-829-110-3 Sequence 3, Appli
8	140.5	15.7	168	3	US-09-134-001C-4664 Sequence 4664, Ap
9	113.5	12.7	162	4	US-09-602-777A-362 Sequence 362, App
10	113	12.7	168	4	US-09-543-681A-7822 Sequence 7822, Ap
11	96.5	10.8	173	3	US-08-818-112-82 Sequence 82, Appli
12	96.5	10.8	173	3	US-08-818-111-83 Sequence 83, Appli
13	96.5	10.8	173	3	US-09-056-556-82 Sequence 82, Appli
14	96.5	10.8	173	4	US-09-072-596-83 Sequence 83, Appli
15	96.5	10.8	173	4	US-09-072-967-82 Sequence 82, Appli
16	96.5	10.8	181	4	US-09-050-733-54 Sequence 54, Appli
17	87	9.7	615	4	US-09-805-455-2 Sequence 2, Appli
18	83	9.3	709	4	US-09-949-016-6809 Sequence 6809, Ap
19	83	9.3	728	4	US-09-949-016-7213 Sequence 7213, Ap
20	82.5	9.2	534	4	US-09-248-796A-15937 Sequence 15937, A
21	81.5	9.1	1332	4	US-09-270-767-59785 Sequence 59785, A
22	81.5	9.1	1607	4	US-09-270-767-44362 Sequence 44362, A
23	80.5	9.0	337	4	US-09-252-991A-17436 Sequence 17436, A
24	79.5	8.9	1057	4	US-09-428-156B-2 Sequence 2, Appli
25	79	8.8	741	4	US-09-949-016-11523 Sequence 11523, A
26	79	8.8	741	4	US-09-949-016-11524 Sequence 11524, A
27	77.5	8.7	1001	3	US-09-060-410-2 Sequence 2, Appli

28	77.5	8.7	1001	4	US-09-723-458-2 Sequence 2, Appli
29	77	8.6	349	3	US-09-459-774-2 Sequence 2, Appli
30	77	8.6	349	4	US-09-417-039-7 Sequence 7, Appli
31	77	8.6	349	4	US-09-903-817-2 Sequence 2, Appli
32	77	8.6	372	4	US-09-949-016-8710 Sequence 8710, Ap
33	76.5	8.6	608	4	US-09-805-455-6 Sequence 6, Appli
34	76	8.5	182	4	US-09-252-991A-17493 Sequence 17493, A
35	76	8.5	462	4	US-09-949-016-6750 Sequence 6750, Ap
36	76	8.5	626	4	US-09-949-016-6749 Sequence 6749, Ap
37	76	8.5	778	4	US-09-949-016-6210 Sequence 6210, Ap
38	75.5	8.5	1037	4	US-09-252-991A-25361 Sequence 25361, A
39	75	8.4	432	4	US-09-583-110-4367 Sequence 4367, Ap
40	75	8.4	434	4	US-09-107-433-3684 Sequence 3684, Ap
41	74.5	8.3	786	4	US-09-688-188B-23 Sequence 23, Appli
42	74.5	8.3	786	4	US-09-291-417D-23 Sequence 23, Appli
43	74.5	8.3	787	4	US-09-688-188B-151 Sequence 151, App
44	74.5	8.3	787	4	US-09-291-417D-151 Sequence 151, App
45	74.5	8.3	1001	4	US-09-688-188B-31 Sequence 31, Appli

ALIGNMENTS

RESULT 1

US-09-949-016-10773  
; Sequence 10773: Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10773  
; LENGTH: 220  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-10773

Query Match 68.9%; Score 615.5; DB 4; Length 220;  
Best Local Similarity 84.6%; Pred No. 1.6e-61;  
Matches 121; Conservative 3; Mismatches 6; Indels 13; Gaps 2;

QY 1 MTTASTQVRQNYHQDSEAAINRQINLELYASVYVLSMSYVDFDRDDVALKNFAKYFLHQ 60  
Db 38 MTTASTQVRQNYHQDSEAAINRQINLELYASVYVLSMSYVDFDRDDVALKNFAKYFLHQ 97

QY 61 HEERQHAELKMLQNGRGRIFLDIKKPCDDWESGLNAMECALHLEKNVQSLLEFPS 120  
Db 98 HEERQHAELKMLQNGRGRIFLDIKKPCDDWESGLNAMECALHLEKNVQSLLEFPS 155

QY 121 PISPSPCSWHYTTNRPOQHHL 143  
Db 156 -----HKLATKNDP---HL 167

RESULT 2

US-09-919-039-333  
; Sequence 333: Application US/09919039  
; Patent No. 6727066  
; GENERAL INFORMATION:  
; APPLICANT: Kaser, Matthew R.  
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES  
; FILE REFERENCE: PA-0035 US

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; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 333
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 4005778CD1
US-09-919-039-333

Query Match          35.4%; Score 316; DB 4; Length 175;
Best Local Similarity 53.6%; Pred. No. 9.4e-28;
Matches 60; Conservative 22; Mismatches 30; Indels 0; Gaps 0;

Qy 6 TSQVRQNYHQDSEAAINRQINLELYASYVYLSMSYFFDRDDVALKXNFAKFLHQSHHEEQ 65
Db 2 SSQIRQNYSTDEAAVNSLVNLYLQASYTYLSLGFYFDRDDVALEGVSHFFRELAEKRE 61

Qy 66 HAEKMLKQNRQGRGRIFLQDIKKPDCDWESGLNAMECALHLEKKNVNSLLE 117
Db 62 GYERLLKQNRQGRGRIFLQDIKKPDCDWESGLNAMECALHLEKKNVNSLLE 113

RESULT 3
US-09-949-016-10295
; Sequence 10295, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10295
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10295

Query Match          34.9%; Score 312; DB 4; Length 238;
Best Local Similarity 52.7%; Pred. No. 4.1e-27;
Matches 59; Conservative 22; Mismatches 31; Indels 0; Gaps 0;

Qy 6 TSQVRQNYHQDSEAAINRQINLELYASYVYLSMSYFFDRDDVALKXNFAKFLHQSHHEEQ 65
Db 65 SSQIRQNYSTDEAAVNSLVNLYLQASYTYLSLGFYFDRDDVALEGVSHFFRELAEKRE 124

Qy 66 HAEKMLKQNRQGRGRIFLQDIKKPDCDWESGLNAMECALHLEKKNVNSLLE 117
Db 125 GYERLLKQNRQGRGRIFLQDIKKPDCDWESGLNAMECALHLEKKNVNSLLE 176

RESULT 4
US-09-418-830-2
; Sequence 2, Application US/09418830
; Patent No. 6563019
; GENERAL INFORMATION:
; APPLICANT: Deak, Maria
; APPLICANT: Dudits, Denes
; APPLICANT: Torok, Karolyne
; APPLICANT: Sass, Laszlo
; APPLICANT: Barna, Balazs
; APPLICANT: Kiraly, Zoltan
; TITLE OF INVENTION: STRESS AND PATHOGEN RESISTANT PLANTS
; FILE REFERENCE: DEAK
; CURRENT APPLICATION NUMBER: US/09/418,830
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: HU 9700762
; PRIOR FILING DATE: 1997-04-16
; PRIOR APPLICATION NUMBER: HU 9700762
; PRIOR FILING DATE: 1997-09-22
; PRIOR APPLICATION NUMBER: HU 9700762
; PRIOR FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01108
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: we do not have
; OTHER INFORMATION: this information
US-09-418-830-3

Query Match          32.9%; Score 294; DB 4; Length 250;
Best Local Similarity 55.8%; Pred. No. 4.8e-25;
Matches 67; Conservative 11; Mismatches 38; Indels 4; Gaps 2;
```

```
; APPLICANT: Torok, Karolyne
; APPLICANT: Sass, Laszlo
; APPLICANT: Barna, Balazs
; APPLICANT: Kiraly, Zoltan
; TITLE OF INVENTION: STRESS AND PATHOGEN RESISTANT PLANTS
; FILE REFERENCE: DEAK
; CURRENT APPLICATION NUMBER: US/09/418,830
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: HU 9700762
; PRIOR FILING DATE: 1997-04-16
; PRIOR APPLICATION NUMBER: HU 9700762
; PRIOR FILING DATE: 1997-09-22
; PRIOR APPLICATION NUMBER: HU 9700762
; PRIOR FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01108
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Medicago sativa
US-09-418-830-2

Query Match          32.9%; Score 294; DB 4; Length 250;
Best Local Similarity 55.8%; Pred. No. 4.8e-25;
Matches 67; Conservative 11; Mismatches 38; Indels 4; Gaps 2;

Qy 5 STSQVRQNYHQDSEAAINRQINLELYASYVYLSMSYFFDRDDVALKXNFAKFLHQSHHEEQ 64
Db 77 NVSLARQNYQDEVSAINEQINVEYNVSYVYHSLFAYFDRDVALKGLAKFKESSESEER 136

Qy 65 QHAEKMLKQNRQGRGRIFLQDIKKPDCDWESGLNAMECALHLEKKNVNSLLEPPS 120
Db 137 EHAELKMKYQNRGVRVHPIVSPPEFDRHAEKGDALYAMELALSLEKLVNEKLVNHS 196
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RESULT 5
US-09-418-830-3
; Sequence 3, Application US/09418830
; Patent No. 6563019
; GENERAL INFORMATION:
; APPLICANT: Deak, Maria
; APPLICANT: Dudits, Denes
; APPLICANT: Torok, Karolyne
; APPLICANT: Sass, Laszlo
; APPLICANT: Barna, Balazs
; APPLICANT: Kiraly, Zoltan
; TITLE OF INVENTION: STRESS AND PATHOGEN RESISTANT PLANTS
; FILE REFERENCE: DEAK
; CURRENT APPLICATION NUMBER: US/09/418,830
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: HU 9700762
; PRIOR FILING DATE: 1997-04-16
; PRIOR APPLICATION NUMBER: HU 9700762
; PRIOR FILING DATE: 1997-09-22
; PRIOR APPLICATION NUMBER: HU 9700762
; PRIOR FILING DATE: 1998-03-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01108
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: we do not have
; OTHER INFORMATION: this information
US-09-418-830-3

Query Match          32.9%; Score 294; DB 4; Length 250;
Best Local Similarity 55.8%; Pred. No. 4.8e-25;
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Matches 67; Conservative 11; Mismatches 38; Indels 4; Gaps 2;
QY 5 STSQVRQNYHDSAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYFLHQSHERR 64
Db 77 NVSLARQNYQDEVSAINEQINVEYNVSYVYLSLFPAYFDRDVALKGLAKFFKESSEER 136
QY 65 OHAELKMLQNRQGRIFLQDIKFP--DCDDWESG--LNAMECALHLEKKNVNSLLEPPS 120
Db 137 EHAELKMLQNRQGRVVRVHLFIVSPSPFDRHAEKGDALYAMELASLSLEKLVNEKLLNVHS 196

RESULT 6
US-09-621-976-4402
; Sequence 4402, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4402
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-4402

Query Match 32.9%; Score 293.5; DB 4; Length 107;
Best Local Similarity 53.8%; Pred. No. 1.7e-25;
Matches 56; Conservative 19; Mismatches 24; Indels 5; Gaps 2;
QY 38 MSYFDRDDVALKNFAKYFLHQSHERRQHAELKMLQNRQGRIFLQDIKPKDCDDWESG 97
Db 1 MAFFERDDVALEHGRIFLHQSDKQHAELMRLQNRGRICLHDIREPQROGWSG 60
QY 98 LNAMECALHLEKKNVNSLLEPPSP--SPSPSC---WHYTTNR 136
Db 61 LEAMECAPHLEKSINYSLELHQLALEKGEPSCATSWRATTLHQ 104

RESULT 7
US-08-829-110-3
; Sequence 3, Application US/08829110
; Patent No. 5882890
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL REGULATORS OF G-PROTEIN
; TITLE OF INVENTION: SIGNALING
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,110
; FILING DATE: Filed Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
```

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; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0259 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 243 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THYMNOT02
; CLONE: 343504
US-08-829-110-3

Query Match 19.8%; Score 177; DB 2; Length 243;
Best Local Similarity 36.0%; Pred. No. 8.1e-12;
Matches 45; Conservative 19; Mismatches 41; Indels 20; Gaps 3;
QY 6 TSQVRQNYHDSAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYFLHQSHERRQ 65
Db 2 SSQIRQNYSTDVEAAVNSLVNLYLOASTYLSLGLFYFDRDDVALEGVSHFFRELAEEAAQ 61
QY 66 HAEKMLQNRQGRIFLQDIK---KPCDDWESGLNAMECALHLEKNVN-----OSLLE 117
Db 62 -----GLRASPEDAKPAWRPPSDIHDSGSSSSHQSLKSTAKWAASLENLLE 109
QY 118 FPSPI 122
Db 110 DPEGV 114

RESULT 8
US-09-134-001C-4664
; Sequence 4664, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4664
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4664

Query Match 15.7%; Score 140.5; DB 3; Length 168;
Best Local Similarity 32.6%; Pred. No. 6.5e-08;
Matches 31; Conservative 23; Mismatches 38; Indels 3; Gaps 2;
QY 19 AAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYFLHQSHERRQHAELKMLQNRG 78
Db 10 AALNEQNMQYFAAHAYMAAAYCDKE--SYDGFANFYIEQAKBERPHGKIIYINDRG 67
QY 79 GRIFLQDIKPKDCDDWESGLNAMECALHLEKNVQ 113
Db 68 EHAIFDTIKAPKV-EFSSILETFKDSLAQERDVTQ 101

RESULT 9
US-09-602-777A-362
; Sequence 362, Application US/09602777A
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Query Match      10.8%; Score 96.5; DB 3; Length 173;
Best Local Similarity 29.7%; Pred. No. 0.0065;
Matches 30; Conservative 19; Mismatches 41; Indels 11; Gaps 3;

QY      19 AAINRQINLELYASYVYLSYYFDRDDVALKNFAKVFHLQSHSEEROHAELKMKLQNRG 78
Db      5 ALMQEQIHNEFTAAQYVAIAVYFDSED--LPQLAKHFYSQAVERNHAMMLVQHLLDRD 62

QY      79 GRIFLODIKKPCD----DWESGLNAMECALHLEKNVNSL 115
Db      63 LRVEI-----PGVDTVRNQFDRPREALALALDQERTVTDQV 98

RESULT 13
US-09-056-556-82
; Sequence 82, Application US/09056556
; Patent No. 6350456
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND
; NUMBER OF SEQUENCES: 241
; CORRESPONDENCE ADDRESS:
; ADDRESS: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,556
; FILING DATE: 07-APR-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.457
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 173 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-056-556-82

Query Match      10.8%; Score 96.5; DB 3; Length 173;
Best Local Similarity 29.7%; Pred. No. 0.0065;
Matches 30; Conservative 19; Mismatches 41; Indels 11; Gaps 3;

QY      19 AAINRQINLELYASYVYLSYYFDRDDVALKNFAKVFHLQSHSEEROHAELKMKLQNRG 78
Db      5 ALMQEQIHNEFTAAQYVAIAVYFDSED--LPQLAKHFYSQAVERNHAMMLVQHLLDRD 62

QY      79 GRIFLODIKKPCD----DWESGLNAMECALHLEKNVNSL 115
Db      63 LRVEI-----PGVDTVRNQFDRPREALALALDQERTVTDQV 98

RESULT 14
US-09-072-596-83
; Sequence 83, Application US/09072596
; Patent No. 6458366
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.

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